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GS; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0042289; F:MFC class II protein binding; ISS.
GO; GO:0042289; F:MFC class II protein binding; ISS.
GO; GO:0045086; P:Desitive regulation of interleukin-2 biosyn. ..;
GO; GO:0045086; P:T-cell differentiation; ISS.
GO; GO:0045086; P:T-cell selection; ISS.
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R GO; GO:0045089; P:T-cell selection; ISS.
R GO; GO:007109; P:Transmembrane receptor protein tyrosine kin. ..;
R InterPro; IPR00973; CD4 TCA9.
R InterPro; IPR007971; CD4 TCA9.
PRINTS; PR007110; Ig-Tike.
JR Pfam; PF00047; ig; 2.
DR Pfam; PF00047; ig; 2.
DR PANAT; SM00406; GO; I.
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                                                                                                           TWTCTVLQNQKKVEFKIDIV
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MEDLINE-84030930; Pubn
Bernstein K.E., Alexar
"Nucleotide sequence of
F-I haplotype.";
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10-OCT-2003 (Rel. 42, Last annotation update)
1g gamma chain C region.
1g gamma chain C region.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Hill R.L., Lebovitz H.E., Fellows (In) Killander J. (eds.);
Gamma globulins, Nobel symp. 3, pp Stockholm (1967).
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Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
"Heavy chain genes of rabbit IgG: isolation of a cDNA encoding
heavy chain and identification of two genomic C gamma genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                                                                               SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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"Sequence studies on the constant region immunoglobulin G of different allotype.";
Biochem. J. 151:337-349(1975).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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SIMILARITY: Contains 3 immunoglobulin-like domains.
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DE Ig gamma-2
OS Cavia porce
OC Eukaryota;
OC Mammalia;
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                                                          Turner K.J., Cebra J.J.;
Turner K.J., Cebra J.J.;
"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of humonoglobulin-G(2) bromide fragments.";
                                                                                                                                                                                                                                                  MEDLINE-71058471; PubMed=5538606; Birshtein B.K., Hussain Q.Z., Cebra J.J.; "Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). 3. Amino acid sequence of thalf-cystine joining heavy and light chains."; Biochemistry 10:18-25(1971).
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MEDLINE 71058486; PubMed=5538616;
Turner K.J., Cebra J.J.;
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21-JUL-1986 (Rel. 01, Las
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15 gamma-2 chain C region
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Biochemistry 10:9-17(1971)
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Cavia porcellus (Guinea pig).
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RESULT 16
CD4_CERAE STANDARD; PRT; 4
ID CD4_CERAE STANDARD; PRT; 4
AC Q08338; O02805; O77593; Q28217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-MAR-2004 (Rel. 43, Last annotation
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SEQUENCE 329
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Tracey D.E., Cebra J.J.;
"Primary structure of the CH2 hom
antibodies.";
Biochemistry 13:4796-4803(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; 19; 2.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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"Interchain disulfide bridg
Biochemistry 10:26-31(1971)
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InterPro; IPR003597;
InterPro; IPR003006;
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MEDLINE=75036073; Pu
Trischmann T.M., Cel
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VDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG
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EMBL; AF001226; AAB60873.1; -.

R EMBL; AF001228; AAB60875.1; -.

R EMBL; AF057380; AAC55124.1; -.

R EMBL; AF057380; AAC55124.1; -.

R EMBL; AF057380; AAC55124.1; -.

R EMG; GO:0042101; C:T-cell receptor complex; ISS.

GO; GO:0042289; F:WHC class II protein binding; ISS.

GO; GO:0042289; F:WHC class II protein binding; ISS.

GO; GO:0045086; P:positive regulation of interleukin-2 bio

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

R GO; GO:0045086; P:T-cell selection; ISS.

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R GO; GO:0045089; P:T-cell selection; ISS.

R GO; GO:0045089; P:T-cell selection; ISS.

R GO; GO:007169; P:transmembrane receptor protein tyrosine

R InterPro; IPR000573; CD4 TCAg.

R InterPro; IPR003596; Ig_v.

R Pfam; PF00047; ig; 2.
PRINTS;
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Harris E.E., Disotell T.R.;
"Nuclear gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corbet S., Barre-Sinoussi F., Allan J.S.;
Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4
"Relation between phylogeny of African green monkey CD4
"Their respective simian immunodeficiency virus genes.";
"J. Med. Primatol. 26:120-128(1997).
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NCBI_TaxID=9534;
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MEDLINE=98017879; PubMed=9379478;
Fomegaard A., Mueller-Trutwin M.C., Diop O., Hansen
Corbet S., Barre-Sinoussi F., Allan J.S.;
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"Cloning and sequences of primate CD4 molecules: diversity
cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93049640; PubMed=1425921;
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Eur. J. Immunol. 22:2973-2981(1992).
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Craniata; Vertebrata; Eutele
Catarrhini; Cercopithecidae;
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MEDLINE=82222190; PubMed=6283537;
Marai S., Nakai S., Miyata Tyamawaki-Kataoka Y., Nakai S., Nakai

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SEQUENCE

OF 335-378 FROM N

79:2623-2627 (1982)

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi; ; Murinae; Mus

Mus.

NCBI_TaxID=10090;

Ig gamma-2B chain C Mus musculus (Mouse)

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                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50835; IG_LIKE; 1.
bulin domain; Transmembrane; Glycoprotein;
                                                                                                                                                                                              TWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                   TWTCTVSQDQNTVEFKIDIM
                                                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSG
                                                                                                                                                                                                                                                                                   MNWGIPFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKTTTQFHWKNSNQIK
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                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                         32.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Lipoprotein; Palmitate.
BY SIMILARITY.
T-CELL SURFACE GLYCOPROTEIN
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                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

S-palmitcyl cysteine (By similarity).

S-palmitcyl cysteine (By similarity).

S-palmitcyl cysteine (By similarity).

K -> N (IN REF. 2 AND 3; AAB60875).

I -> T (IN REF. 3; AAB60873).

K -> E (IN REF. 3; AAB60873).

G -> V (IN REF. 3; AAB60873).

M -> V (IN REF. 3; AAB60873).

K -> E (IN REF. 3; AAB60873).

K -> E (IN REF. 3; AAB60873).

K -> H (IN REF. 3; AAB60873).

K -> H (IN REF. 3; AAB60873).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                  Score 885; DB Pred. No. 1.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
N-LINKED
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(GLCNAC.)
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Pfam; PF00047; Igc1; 2.

SMART; SM00407; IGc1; 2.

PROSITE; PS00289; IG_MHC; 1.

Immunoglobulin domain; Immunoglobulin C region; Transmembrane;

Alternative splicing; 3D-structure; Repeat.
                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rogers J., Ch
Eisenberg D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thie
                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; C02154; G2MSBM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=82115295; PubMed=6799207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WGD; MGI:96445; Igh-3.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene segments encoding transmembrane carboxyl termini of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    identical with the corresponding region of the secreted form. MISCELLANEOUS: The a allele sequence is shown. SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=Membrane-bound;
IsoId=P01867-1; Sequence=Displayed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1CIC; 11-MAR-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration -
sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                        133
                                              229
                                                                                             183
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                                                                       78
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M: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS SCELLANEOUS: The sequence of residues 1-335 is assumed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P01866-1; Sequence=External;
                                                                                                                                                                              Similarity
SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
                                   PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                                                                    QTVTCSVAHPASSTTVDKKLEPSGPISTINPCP----PCKECHKCPAPNLEGGPSVFIF
                                                                                          ---TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTC--PELLGGPSVFLF
                                                                                                                   LVKGYFPESVTVTWNSGSLSSSVHTFPAL-----LQSG-LYTMSSSVTVPSSTWPS
                                                                                                                                         LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                      PPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVV
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                                                                                                                                                                              32.5%;
51.7%;
                                                                                                                                                                                                               MW;
                                                                                                                                                                 52;
                                                                                                                                                                                                                                                                       INTERCHAIN
INTERCHAIN
INTERCHAIN
INTERCHAIN
                                                                                                                                                                             Score 877.5;
Pred. No. 4.
                                                                                                                                                                                                                          POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                           IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
                                                                                                                                                                                                                                                                                                                                INTERCHAIN
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                                                                                                                                                                                                              89B3CF0A9B6D49FA CRC64;
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_HIKE; 3.
PROSITE; PS90290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M., Tucker P.W., Blattner F.R.;
"Structural analysis of the murine IgG3 constant region gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Last sequence 16-OCT-2001 (Rel. 40, Last annotation of gamma-3 chain C region, secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P22436;
01-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; ig; 3.
SMART; SM00407; IGc1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B02156; (
HSSP; P01857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J00451; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 3:2041-2046(1984)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; Alternative splicing
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                                                                                                                                                                                                                                                     162;
                                                                                                                                                               62
                                                                                                                                                                                                                                                                          Similarity
LGGPSVFLFPPXPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
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                                                                                                                                                             SLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPRIPKPSTPPGS-----
                                                                                                                                                                                                       SVSQLELQDSGTW----TCTVLQNQKKVEFKIDI---VPCPAPEPKSCDKTHTCP--EL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SITCIVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF 408
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329 AA;
                                                                                                                                                                                                                                                     Conservative
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223 CH
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36228 MW;
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Ig_cl.
Ig_MHC.
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                                                                                                                                                                                                                                                     38;
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CH2.
CH3.
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Pred. No. 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
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Best Local Sim:
Matches 157;
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NON TER 1

DOMĀIN 124

DOMAIN 232

DISULFID 155

DISULFID 106

DISULFID 109

DISULFID 102

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DISULFID 125
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P20761;
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; 19; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; PS0018; PS0018.
HSSP; P01842; 7FAB.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brueggemann M.;
"Evolution of the rat immunoglobulin gamma heavy-chain gene
Gene 74:473-482(1988).
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig gamma-2B chain C region.
Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata; Craniata; Verte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=89232738; PubMed=3149946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                              Local Similarity
 245
                     344
                                            185
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                                         SGTW-----TCTVLQ--NQKKVEFKIDI-----VPCPAPEPKSCDKTHTC--PELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                      SVFIFPPKPKDILLISQNAKVTCVVVDVSEEEPDVQFSWFVNNVEVHTAQTQPREEQYNS
                                                                                                  SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
TEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLNVERSRWD
           TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ
                                                                                                                                    SSTWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCP----TCPTCHKCPVPELLGGP
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
                                                                                                                                                                                             Score 833;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                              55F8B64D48D460A6 CRC64;
                                                                                                                                                                                  Mismatches
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HLIM)
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HLIM)
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Matches 163
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InterPro; IPR003597; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE:
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P20759;
01-FEB-1991
01-FEB-1991
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NON TER 1
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DOMAIN
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01-FEB-1991 (Rel. 17, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig gamma-1 chain C region.
Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 74:473-482(1988)
PIR; PS0017; PS0017.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brueggemann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89232738;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Evolution of the rat
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240
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                                                                                                                                                                                                163;
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                                                                                                                                                                                                          Similarity
                                                                                                                              LVXGYFPEPVTVTWNSGALSSGVHTFPAV-----LQSGLYTLTSSVTV-PSSTWPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                               RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
                                                                                                                  QTVTCNVAHPASSTKVDKKI------VPRNC-----GGDCKPCICTGSEVSSV
                                                                                                                                                                            LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                                                                                       FLFPPKDKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY
NEVSITCMVKGFYPPDIYVEWQMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKEKWQQG
                                     RSVSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMSPTKEEMTQ
                                                                            FIFPPKPKDVLTITLTPKVTCVVVDISQDDPEVHFSWFVDDVEVHTAQTRPPEEQFNSTF
                                                                                                                                                                                                 Conservative
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50.0%;
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INTERCHAIN
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HINGE.
CH2.
CH3.
                                                                                                                                                                                                        Score 823.5; DB 1;
Pred. No. 1e-45;
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013BAB45EF49B9DA CRC64;
                                                                                                                                                                                                 Mismatches
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CHAIN)
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                  405
                                                         345
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Best Local S
Matches 151
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DISULFID
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Brueggemann M., Delmastro-Galfre P., Waldmann H., Ci
"Sequence of a rat immunoglobulin gamma 2c heavy cha
region cDNA: extensive homology to mouse gamma 3.";
Eur. J. Immunol. 18:317-319(1988).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; 1g; 2.
SMART; SM00407; IGc1; 2.
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PIR; S00847; S00847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1999 (Rel. 38, Last annotation Ig gamma-2C chain C region. Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                DISULFID
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InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
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                                            294
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  191
                                                                                                                                                                       72
                                                                                                                                                                                                                                                                              Similarity
                                   LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCL
QHQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKARTPQVYTIPPPREQMSKNKVSLTCM
                                                                                                         DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                                                       SSTWSSQTVTCSVAHPATKSNLIKRIEP-RRPKPRPPTDICSCODNLGRPSVFIFPPKPK
                                                                                                                                                                                                                 SGTW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50835; iG_LIKE; 3. PS00290; iG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin
                                                                                                                                                                                                                                                                                                                                          MΨ,
                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                      Score 823; DB 1; 1
Pred. No. 1.1e-45;
5; Mismatches 56;
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CH2.
CH3.
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                                                                                                                                                                                                                                                                                             "Evolution of immunoglobulin subclasses. murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
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Honjo T., Obata M., Yamawaki-Kataoka Y.,
Takahashi N., Mano Y.;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis heavy chain.";
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18:559-568(1979)
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MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
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PIR; A02152; G2MSA.
PDB; 124W; 12-JUL-01.
PDB; 1E4X; 12-JUL-01.
PDB; 1MNU; 06-MAY-99.
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PROSITE; PS00299; IG_MHC; 1.
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"Structure of the constant and 3' untranslated
Balb/c gamma Za heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
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MEDLINE=81076554; PubMed=6777755;
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"Determination of the primary structure of a mouse gamm immunoglobulin. Identification of the disulfide bridges Eur. J. Biochem. 30:452-462(1972).
-i- SIMILARITY: Contains 3 immunoglobulin-like domains.
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Bourgois A., Fougereau M., Rocca-
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro; IPR003006; Ig_MHC.
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"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Implier the evolution of immunoglobulin structure and function.
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GCAB MOUSE
ID GCAB MOU
AC PO1864;
DT 21-JUL-1
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ON MUSE TAIAN-C
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Best Local &
Matches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986
21-JUL-1986
15-MAR-2004
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DISULFID
DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=82037861; PubMed=6170065;
Schreier P.H., Bothwell A.L.M., Mueller-Hill B.,
"Multiple differences between the nucleic acid so
IgG2aa and IgG2ab alleles of the mouse.";
Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                           MEDIINE=82037777; PubMed=6794027;
Dognin M.J., Lauwereys M., Strosberg A.D.;
Dognin M.J., Lauwereys M., Strosberg A.D.;
"Multiple amino acid substitutions between murine chain Fc regions of Igla and Iglb allotypic forms.
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-i- SUBCELLULAR LOCATION: Secreted (Potential).
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-2A chain
                                                        Name=Membrane-bound;
IsoId=P0185-1; Sequence=External;
MISCELLANEOUS: The sequence differs from that of the
from BALB/c mice, at 15% of the positions.
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                    Name=Secreted;
                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2,
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                        SWISS-PROT entry is
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                                                                                                                                                                          Note=Probably the major isoform;
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,6 (Rel. 01, Long (Rel. 43, 7) (Rel. 43, 7) (Rel. 43, 7)
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Last annotation update)
region secreted form (B allele)
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copyright. It is produced through a c
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Pred. No. 1.
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B84361C5445A6864 CRC64;
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Sciurognathi; Muridae;
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A HEAVY CHAIN).
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Best Local S
Matches 166
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PIR; A02153; G2MSAB.
PDB; 1BOG; 23-MAR-99.
PDB; 1HH6; 26-JAN-01.
PDB; 1HH6; 26-JAN-01.
PDB; 1HH6; 27-JUL-03.
PDB; 1HH6; 28-FEB-01.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
PROSITE; PR00407; IG; 2.
SMART; SM00407; IGCL; 2.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00835; IG_LIKE; 3.
                                                                                                                         GCA RAT
P20760;
01-FEB-1991
01-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
SEQUENCE
                    SEQUENCE FROM N.A. MEDLINE=89232738;
                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
10-OCT-2003 (Rel. 42, Last ann
1g gamma-2A chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                   NCBI_TaxID=10116;
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                                                                   Chordata;
Rodentia;
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Pred. No. 2.
                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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Brueggemann "Evolution o

of the

rat

immunoglobulin gamma

heavy-chain

gene family.";

PubMed=3149946;

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T-cell surface 9. (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M13804; AAA41376.1; ALT_INIT. PIR; PS0019; PS0019. HSSP; P01842; 7FAB.
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SMART; SM00407; IGc1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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PS50835; IG_LIKE; 3.
PS00290; IG_MHC; 1.
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121 317
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35186 MW;
                                                                     (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 42, Last annotation updat
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Pred. No. 9.4e
17; Mismatches
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IG-LIKE
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                                                    tation update)
(T-cell surface antigen T4/Leu-3)
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REMBL; X73328; CAA51754.1; -.

REMBL; X73327; CAA51753.1; -.

DR HSSP; P01730; 1WIQ.

DR GQ: GG:004210; C:T-cell receptor complex; ISS.

DR GQ: GG:004210; C:T-cell protein binding; ISS.

DR GQ: GG:004289; F:MHC class II protein binding; ISS.

DR GQ: GG:000455; P:immune response; ISS.

DR GQ: GG:00456; P:positive regulation of interleukin-2 biosyn.

DR GQ: GG:0045086; P:T-cell differentiation; ISS.

DR GQ: GG:004508; P:T-cell differentiation; ISS.

DR GQ: GG:004508; P:T-cell differentiation; ISS.

DR GQ: GG:004508; P:T-cell differentiation; ISS.

DR InterPro; IPR00710; IG-Tike.

DR InterPro; IPR00710; IG-Tike.

DR InterPro; IPR00710; IG-Tike.

DR InterPro; IPR00710; IG-Tike.

DR InterPro; IPR003596; IG-V

Pfam: PF00047; IG: 2-V

PFam: PF00047; IG: 2-V

PFam: PF00047; IG: 2-V

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Eur. J. Immunol. 22:93-2981(1992).
-!- FUNCTION: Accessory Protein for WHC class-II antigen/T-cell
    receptor interaction. May regulate T-cell activation.
-!- SUBUNIT: Associates with p56-lck (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin domain; Transmembrane;
Immune response; Repeat; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey) 
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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392
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99
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291
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N-LINKED (GLCNAC...)
N-LINKED GLCNAC...)
N-LINKED GLCNAC...)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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S-palmitcyl cysteine (
MISSING.
T -> I.
V -> M.
V -> M.
R -> K.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                              Glycoprotein; Palmitate.
                                                                                                                                                                                                                                                                         (POTENTIAL).
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(POTENTIAL).
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Q08339;
01-FEB-1995
01-FEB-1995
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                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long. It is content use by non-profit institutions as long as its content use by non-profit institutions as long.
                                        InterPro; IPR000973; CD4 TCAG
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erythrocebus patas (Red guenon) (Hussar).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 (T-cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93049640;
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                                                                                                               GO:0042101; C:T-cell receptor complex; ISS.
GO:0042109; F:Goreceptor activity; ISS.
GO:0042209; F:MC class II protein binding; ISS.
GO:0042209; F:MC class II protein binding; ISS.
GO:0045056; P:immune response; ISS.
GO:0045056; P:positive regulation of interleukin-2
GO:0030217; P:T-cell differentiation; ISS.
GO:0045058; P:T-cell selection; ISS.
GO:007109; P:transmembrane receptor protein tyrosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity).
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                                                                                                                                                                                                                                                                                                                                               X73324;
P01730;
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  CD4TCANTIGEN
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Pred. No. 4.3e-43;
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15-MAR-2004 (Rel.
Ig gamma-2B chain
                           21-JUL-1986
15-MAR-2004
                                              21-JUL-1986
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Immune response; Repeat; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                     Similarity
                                                                                                               GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIV
                                                                                                                          GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                                                                                                   DQGCFSMIIKNLKIEDSETYICEVEDKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP
                                                                                                                                                                DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESSP 147
                                                                                                                                                                                      VVLGKKGDTVELTCNASQKTTTQFHWKNSNQMKILGKQGSFLTKGPSKLRDRTDSRKSLW
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3_LIKE; 1.
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BY SIMILARITY.
S-palmitoyl cystein
S-palmitoyl cystein
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CYTOPLASMIC (POTENT
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                    Score 783; DB 1;
Pred. No. 4.9e-43;
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                           update)
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Tucker P.W., Marcu K.B., Newell N., F
"Sequence of the cloned gene for the
2b immunoglobulin heavy chain.";
Science 206:1303-1306(1979).
                                   Tucker P.W., Marcu K.B., Slightom J.L., Blattnu "Structure of the constant and 3' untranslated gamma 2b heavy chain messenger RNA.";
                                                                                                                                                                             Yamawaki-Kataoka Y., Kataoka T., "Complete nucleotide sequence of cloned from newborn nouse DNA.";
                                                                                                                                 SEQUENCE FROM N.A. (MPC 11).
MEDLINE=80081501; PubMed=117548;
                                                                                                                                                                                                   SEQUENCE FROM N.A. (ALLELE A).
MEDLINE=80120716; PubMed=6766534;
Yamawaki-Kataoka Y., Kataoka T.,
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                         Science
                                                                                                                                                                     Nature
                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                    from newborn nouse 283:786-789(1980).
                                                                                       heavy chain messenger
206:1299-1303(1979).
                                                                                                                                                                                                                                                         Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                             Richards J.,
                                  constant
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                                              Blattner F.R.;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 3.
PROSITE; PS00835; IG_LIKE; 3.
PROSITE; PS00835; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Repeat.
                                                                                                                                                                                                                                                                                                                                            DOMĀIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94216359; PubMed=7512967; Krim H., Yamaguchi Y., Masuda K., Matsunaga Irimura T., Takahashi N., Kato K., Arata Y "O-glycosylation in hinge region of mouse J. Biol. Chem. 269:12345-12350(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2a and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ollo R., Rougeon F.;
"Mouse immunoglobulin allotypes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01842; 7FAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS MISCELLANEOUS: The a allele sequence is shown.
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId-P01866-1; Sequence-Displayed;
Note-May be the major isoform;
Name-Membrane-bound;
IsoId-P01867-1; Sequence-External;
PTM: O-LINKED GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH MODIFIED WITH 2 SIALIC ACID RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted (Potential). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S25057; G2MS11.
 229
                                        183
                                                                                                    161;
                    78
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296:761-763(1982).
                                                                                                               Similarity
PPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV
                    QTVTCSVAHPASSTTVDKKLEPSGPISTINPCP----PCKECHKCPAPNLEGGPSVFIF
                                       ---TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTC--PELLGGPSVFLF
                                                            LVKGYFPESVTVTWNSGSLSSSVHTFPAL-----LQSG-LYTMSSSVTVPSSTWPS
                                                                                LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
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I -> P
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Pred. No. 5e-
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., Arata Y.
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R (IN ALLELE B).
D (IN ALLELE B).
D (IN ALLELE B).
G (IN ALLELE B).
S (IN REF. 2 AND 3).
P (IN REF. 2 AND 3).
T (IN REF. 2 AND 3).
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N ALLELE B).
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N ALLELE B).
N REF. 2 AND 3).
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                                                                                                                       DB 1;
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RESULT
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SMART; S
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GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:00162289; F:MHC class II protein binding; ISS.
GO; GO:0006955; P:immune response; ISS.
GO; GO:0045086; P:positive response; ISS.
GO; GO:0045086; P:positive regulation of interleukin-2
GO; GO:0045086; P:T-cell differentiation; ISS.
GO; GO:0030217; P:T-cell selection; ISS.
GO; GO:004508; P:T-cell selection; ISS.
                                                                                                                                                                                                                                                                                                                                                              entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q29037;
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01-NOV-1997 (Rel. 42, Last a:
10-OCT-2003 (Rel. 42, Last a:
                                                                                                                                                                                                                                                                                                                                   EMBL; D86588; BAA13131.1; -. HSSP; P01730; 1WBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor interaction. May regulate T-cell activation.
-! SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tatsumi M., Hashimoto O. Submitted (AUG-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saimiri sciureus (Common squirrel monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae;
                                                             SIGNAL
                                                                                                                                                                InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: Accessory protein for MHC class-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9521;
                                                                            Immune
                                                                                           [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409
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                                                                                                                    ; PR00692; CD4TC;
SM00406; IGV; 1
                                                                                       PS50835; IG_LIKE; 1.
obulin domain; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTIRVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLTCLVVGFNPGDISVEWTSNGHTEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLPIQHQDWMSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDV
                                                                                                                                                     <u>, 6</u>1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
Repeat; Signal; Lipoprotein; Palmitate.

25 BY SIMILARITY.

457 T-CELL SURFACE GLYCOPROTEIN

395 EXTRACELULAR (POTENTIAL).

417 POTENTIAL.

457 CYTOPLASMIC (POTENTIAL).
                                                                                                                                       CD4TCANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
protein CD4 precursor (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tation update)
precursor (T-cell surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   431
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                                                                                                                                                                                                             tyrosine kin.
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                                                                                           T-cell;
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Cebinae; Saimiri.
                                                                                                                                                                                                                                                         biosyn.
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Best Local S
Matches 205
                                                                                                          CD4_CANFA STANDARD;
P33705;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last set
15-MAR-2004 (Rel. 43, Last and
T-cell surface glycoprotein Cl
                                                                                                                                                                                 CANFA
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SEQUENCE
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CARBOHYD
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DISULFID
DISULFID
DISULFID
                                                     Canis familiaris (Do
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                    T4/Leu-3).
SEQUENCE OF 13-463 FROM N.A. STRAIN=Beagle; TISSUE=Thymus; MEDLINE=93192324; PubMed=7916
                                        NCBI_TaxID=9615;
                                                                                                                                                                                                                            387
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                                                                                                                                                                                                                                                                                  HYTQKSLSLSPGLQLDETCAEAQDGELDGLWTTDP-PRASALPAPPTGSALPDPQTASAL
                                                                                                                                                                                                                                                                                                                                                             --QDPKLRMGKK---LPLHLTLAQALPQYAGSGNFTL-------ALKG---
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                                                                                                                                                                                                                            PTRSPPVQ---PMVLIVLGGVAGLLAFTGLGIFLCVRCRHR
                                                                                                                                                                                                                                                 P--DPPAASALPAALAVISFLIGL----GLGV-ACVLARTR
                                                                                                                                                                                                                                                                       --TSPKLMLS
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                                                      ; (Dog).
coa; Chordata; C
cia; Carnivora;
                                                                                                 28, Created,
28, Last sequence update)
43, Last annotation update)
vcoprotein CD4 precursor (T-cell
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202
202
316
373
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254
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1184
4184
4218
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
N-LINKED (GLCNAC. ..)
SY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
S-palmitoyl cysteine (
S-palmitoyl cysteine (
S-palmitoyl cysteine (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 743; DB 1;
Pred. No. 2.1e-40;
5; Mismatches 150
                                                     Craniata; Vertebrata;
; Fissipedia; Canidae;
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                  ----GKLHQEVNLVVMRVTQLQNNL-TCEVWGP----
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                                                                  Euteleostomi,
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similarity)
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Query Match
Best Local S
Matches 177
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GO; GO:0042101; C:T-cell receptor activity; ISS.
GO; GO:0042108; F:MCCclass II protein binding; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:00069555; P:immune response; ISS.
GO; GO:00069555; P:T-cell differentiation; ISS.
GO; GO:0045086; P:T-cell selection; ISS.
GO; GO:0046; ISS.
GO; GO:00
                                                                                                                                    LIPID
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Beagle; TISSUE=Thymus;
MEDLINE=94378217; PubMed=8091416;
Gorman S.D., Frewin M.R., Cobbold S.P., Waldmann H.;
"Isolation and expression of cDNA encoding the canine CD4
alpha antigens.";
Tricons **Tricons**;
                                                                                    CARBOHYD
CARBOHYD
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DISULFID
DISULFID
LIPID
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TRANSMEM
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SIGNAL
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-i- SUBUNIT: Associates with p56-lck (By similarity).
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: Expressed in macrophages and a subset o
                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Antigens 43:184-188(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Milde K.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T lymphocytes.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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P01730; 1WBR.
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X68565; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F., Conner G.E., Minz D.H., Alejandro R structure of the canine CD4 antigen."; Biophys. Acta 1172:315-318(1993).
                                                                  463
423
463
124
221
321
371
378
109
374
424
424
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427
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429
3168
1176
329
389
389
                22.9%;
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t; Signal; Lipoprotein; Palmitate.
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                                                                              POTENTIAL.
CYTOPLASMIC (POTE
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 3
BY SIMILARITY.
BY SIMILARITY.
 Score 617.5; D
Pred. No. 2.2e-
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                T-CELL SURFACE GLYCOPROTE EXTRACELLULAR (POTENTIAL)
                                                                     95805170CB44A833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                  SURFACE GLYCOPROTEIN
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                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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                                                                    CRC64;
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e (By similarity)
.) (POTENTIAL).
                              Length
                                                                                                  ) (POTENTIAL)
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                                                                                     (POTENTIAL
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                                   463;
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6 outstation -
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Similarity

Conservative

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P46630;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell surface
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                             MEDLINE-92390370; PubMed-1518821;
Hague B.F., Sawasdikosol S., Brow
Kindt T.J.;
                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986
                                                                                                                                                                                                                            'CD4 and its role in infection of rabbit cell lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LL-----WISFTLENRKLSMKEAHAPL-----KLQMKESLPLRFTLPQVLSRYAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWPELODGGTWTCIISQSQKTVEFNINVLVLAF---QKVSNTFYARE--GDQVEFSFP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKDTLMISRTPEVTCVVVDVSHEDPEV--KFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILGNOGSFWTVGSSRLKHRVESKKNLWDQGSFPLVIKDLEVADSGIYFCDT-DKRQEVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNQEAAFRHLLLMLQLVMLPAVTPVREVVLGKAGDAVELPCQTSQKKNIHFNWRDSSMVQ
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                                                                                                                                                                                                                                                       Brown T.J.,
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DISULFID
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LIPID
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DOMAIN
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DOMAIN
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GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0042289; F:mMC class II protein binding; ISS.
GO; GO:0046525; P:immune response; ISS.
GO; GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO; GO:0045086; P:r-cell differentiation; ISS.
GO; GO:0030217; P:T-cell selection; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0045058; P:transmembrane receptor protein tyrosine kin.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0692; CD4TC; SMART; SM00406; IGV; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000973; CD4 TCAg. InterPro; IPR007110; Ig-like. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 2.
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Immunoglobulin domain; Tra
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304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  response;
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                                           SAQSWVSFSLEDRKVSVQKILP---DLKIQMSKGLPLS---LTLPQALHRYAGSGNLSLT
                     CLVKG
                                                                                                                                                                         EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
                                                                                                                                                                                                                                              ILGNQG----SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE
-LDKG
                                                                LHQDWLNGKEYKCKVS-NKALPAPIEKTISKAKGQPREPQVYTLPPSRDELT-KNQVSLT
                                                                                                          LMISRTPEVTCVVVDVSHEDPEV--KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                 QDSGTWSCHLSFQDQNKLELDIKIIVLGFPKASA----
                                                                                                                                                      QDSGTWTCTV-LQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                    MNRRIYFQCLLLVLPLALLPAATWGKTVVRGKAGAIVELPCQSSQKRNSVFNWKHANQVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Glycoprotein; T-cell;
                                                                                      -LNFEDESLSGELMWQVDGAS---
                                                                                                                                                                                                                                                                                                                 47;
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
S-palmitoyl cysteine (By similarity).
S-palmitoyl cysteine (By similarity).
; B323311CBD40013D CRC64;
                                                                                                                                                                                                                                                                                                              Pred. No. 2.36
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
T-CELL SUR
                                                                                                                                                                                                                                                                                                                                       Score 601.5;
                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein;
                                                                                                                                                                                                                                                                                                                            No. 2.3e-31
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                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                       459;
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RESULT 32 CD4_RAT

CD4_RAT

STANDARD;

457

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EMBL; M15768; AAA40901.1; -.

PR PIR; A27449; A27449.

R PDB; 1CID; 15-JUL-93.

R GlycoSulteDB; P05540; -.

R GO; GO:0042101; C:T-cell receptor complex; ISS.

R GO; GO:004229; F:MCC class II protein binding; ISS.

GO; GO:0004599; F:MC class II protein binding; ISS.

R GO; GO:0004595; P:immune response; ISS.

R GO; GO:0045086; P:positive regulation of interleukin-2 biosyn...

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0030217; P:T-cell selection; ISS.

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0030217; P:T-cell selection; ISS.

R GO; GO:0007169; P:transmembrane receptor protein tyrosine kin...

R InterPro; IPR0003599; IG.

R InterPro; IPR003599; IG.

R InterPro; IPR003599; IG.
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SEQUENCE FROM N.A., AND FARLE.
SEQUENCE FROM N.A., AND FARLE.
MEDLINE=87175535; PubMede3104900;
Clark S.J., Jefferies W.A., Barclay A.N., Gagnon J.,
"Peptide and nucleotide sequences of rat CD4 (W3/25)
"Peptide and nucleotide sequences of rat CD4 (W3/25)"
"Peptide and nucleo
                                                                                                                                       DOMAIN
TRANSMEM
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DOMAIN
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CHAIN
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01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell T4/Leu-3) (W3/25 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        иве
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brady R.L., Dodson E.J., Dodson G.G., Williams A.F., Barclay A.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93262437; PubMed=8493535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (F
Eukaryota, Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Crystal
                                                                                                                                                                                                                                                       mmunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBCUNIT: Associates with p56-lck (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                     ; PR00692; CD
SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long as its content is d and this statement is not removed. Usage by and for srequires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           structure of
                                                                                                                                                                                                                                                                             PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                         domain;
                                                                                                                                                                                                                                 Repeat;
                                                                                                                                                                                                                                                                                                                             CD4TCANTIGEN
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                                                                                                                                                                                                                               Transmembrane; Glycoprotein; T-cell; Signal; Lipoprotein; Palmitate; 3D
              EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASNIC (POTENTIAL).
IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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Sciurognathi; Muridae;
                                                                                                                                                                                     SURFACE
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(GLCNAC.
                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                   GLYCOPROTEIN
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(POTENTIAL)
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; Murinae; Rat
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RESULT 33
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ID CD4 MOUSE
ID CD4 MOUSE
OF O1-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE T-cell surface glycoprotein CD4 precursor (T-cell furface)
DE T4/Leu-3) (T-cell differentiation antigen L374
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137; Conserv
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                                                                                                                                                                                                                                                                                                      MNRGVPFRHL--LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
                                                                                                            GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                            QSWITFSLKNQKVS--
                                                                                                                                          QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK
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                                                                                                                                                                                                                           ELWVFRVTFNPGTRLLQGQSLTLILDSNPKVSDPPIECKHKSSNIVKDSKAFSTHSLRIQ
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N-LINKED (GLCNAC...)
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S-palmitoyl cysteine (
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antigen L3T4)

(T-cell

Burface

antigen

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIJUE-98112780; PubMed=9445485;
Ansari-Lari M.A., Oeltjen J.C., Schwartz
Lu J., Gorrell J.H., Chinault A.C., Belmc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Unusual intron in the immunoglobulin domain of the newly isolated murine CD4 (L3T4) gene."; Nature 325:453-455(1987).
                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE-Mammary gland;
MEDLINE-22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparative sequence analysis of chromosome 12pl3 and its syntenic Genome Res. 8:29-40(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=88152875; PubMed=3326818; Parnes J.R., Hunkapiller T.; "L3T4 and the immunoglobulin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=87115821; PubMed=3027575;
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MEDLINE=87018845; PubMed=3094146;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                               SEQUENCE OF 27-43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorman S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88041159; PubMed=2823269;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Isolation and sequence of L3T4 complementary DNA clones: in T cells and brain.";
                                MEDLINE=86166694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorman S.D., Tour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus
=86166694; PubMed=3082751;
B.J., Tsagaratos J., Kirs
M., McKenzie I.F.C., Walk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234:610-614(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM
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                                                                                cDNA sequences.
d. Sci. U.S.A. 9
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Kirszbaum I
Walker I.D.
                                                                                99:16899-16903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a gene-rich cluster at human region in mouse chromosome 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              superfamily: new relationships
nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wartz S., Zhang Z., Muzny D.M.,
Belmont J.W., Miller W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD4 and
               ۲.,
                 Maddox
                                                                                (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an unusual
               ď.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome 6.";
                 McKay
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EMBL; M36850; AAA39401.1; -.
EMBL; M13816; AAA37267; 1; -.
EMBL; M14836; CAA285391; -.
EMBL; M36851; AAA39402.1; -.
EMBL; M17080; AAA37403.1; -.
EMBL; M17078; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; M17079; AAA37403.1; JOINED.
EMBL; AC002397; AAC36610.1; -.
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-!- ALTERNATI
 TRANSMEM
DOMAIN
DOMAIN
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CARBOHYD
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                                                                                                                                                                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
Pfam; PF00047; ig; 2.
PRINTS; PRONECT
                                                                                                                                                                                                                                                                                                     GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0045289; F:immune response; ISS.
GO; GO:0045086; P:positive regulation of interleukin-2 biosyn...
GO; GO:0045086; P:T-cell differentiation; ISS.
GO; GO:0045058; P:T-cell differentiation; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0007169; P:transmembrane receptor protein tyrosine kin...
Interpro; IPR000973; CD4 TCA9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC039137; AAH39137.1; -. PIR; A02110; RWMST4
                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outsut the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Classon B.J., Tsagaratos J., McKenzie I.F.C., Wall
"Partial primary structure of the T4 antigens of is
assignment of intrachain disulfide bonds.",
Proc. Natl. Acad. Sci. U.S.A. 83:4499-4503(1986).
                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                  SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A02110; RWMST4.
HSSP; P01730; 1WBR.
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                                                                                                                                  DOMAIN
                                                                                                                                                                          Alternative
                                                                                                                                                                                     Immunoglobulin domain; Transmembrane; Glycoprotein; T-cell; Immune response; Repeat; Signal; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The L3T4 antigen in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Accessory protein for MHC class-II antigen/receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2; Synonyms=Brain-specific;
IsoId=P06332-2; Sequence=VSP 002489;
SIMILARITY: Contains 3 immunoglobulin-like
SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:88335;
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                                        IG-LIKE V-TYPE.
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                  EXTRACELLULAR POTENTIAL.
CYTOPLASMIC (P
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N-LINKED
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                                                                                                                                              GLYCOPROTEIN
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V-type domain.
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RESULT 34

EPC MOUSE

ID EPC MOUSE

TO 196336; P01856;

DT 21-JUL-1986 (Rel. 01, Created Pot 21-JUL-1986 (Rel. 33, Last as 1 19 pepsilon chain C region.

OE Mammalia; Eutheria; Rodentia.

OC III

RA SEQUENCE FROM N.A.

RX MEDLINE=84236092; PubMed=632;

RA Ishida N., Ueda S., Hayashid;

RT comparison with the human epi
RT SEQUENCE OF 34-421 FROM N.A.

RX MEDLINE=83117774; PubMed=681

RA Honjo T.;

RA Honjo 
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Ishida N., Ueda S., Hayashida H., Miyat
"The nucleotide sequence of the mouse i
comparison with the human epsilon gene
EMBO J. 1:1117-1123(1982).
                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                              SEQUENCE OF 34-421 FROM N.A.
MEDLINE=83117774; PubMed=6818553;
Liu F.-T., Albrandt K., Succliffe
"Cloning and nucleotide sequence c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR
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annotation update)
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                                                                                                          agreement (See http://www.isb-sib.
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Pred. No. 2.8e
32; Mismatches
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S-palmitoyl cysteine
Missing (in isoform 2
/FTId=VSP_002489.
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RESULT 35
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SMART; SM00407; IGc1; 2
  Homo sapiens
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PROSITE; PS00290; IG_MHC; 3.
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HSSP; P01854; 1IGE
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                                                                                                           HSTTTP-LKSNGSNQGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPRKLEKTISTSLG
                                                                                                                                             SASQWY---TKHHN------NATTSITSITPVVAKDWIEGYGYQCIVDHPDFPKPI
                                                                                                                         YKTTPPVLDSDGS---FFLYSKLTVDKSRWQQGNVFSCSVMHBALHN-HYTQKSLSLSPG
                                                                                                                                                                                             ----WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
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n C region.
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  (Human)
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Ig_c1.
Ig_MHC.
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                           sequence update) annotation updat
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BY SIMILARITY.
N-LINKED (GLCN)
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Pred. No. 9e-18;
7; Mismatches 1
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Interpro, ..., 19; 4. Pfam; PF00047; 19; 4. SMART; SM00407; IGc1; 3.
                                                                                            GlycoSuiteDB; P01871; -..
GO; GO:0005624; C:membra
GO; GO:0003823; F:antige
GO; GO:0006955; P:immune
                                                                                                                                                                                EMBL; X17115; CAA34971.1; ALT EMBL; X57086; -; NOT ANNOTATE HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long the content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      chain cDNA from B cells and mouse-human hybridomas.";
Proc. Natl. Acad. Sci. U.S.A. 77:6027-6031(1980)
-i- MISCELLANEOUS: All 4 combinations of the S/G and V/G
at positions 192 and 216 have been observed in human
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Dolby T.W., Devuono J., Croce C.M.;

"Cloning and partial nucleotide sequence of human immunoglobulin
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                                            InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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MEDLINE=82059479; PubMed=6795593;
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MEDLINE=75059123; PubMed=4803843;
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Mammalia; Eutheria;
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"Complete amino acid sequence
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Mihaeeco E., Barnikol-Watanabe S.,
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GO:0003823, F:antigen binding,
GO:0006955, P:immune response,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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RESULT 3
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P01855;
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                                      MEDLINE-82174576; PubMed-6803238; MEDLINE-82174576; PubMed-6803238; Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mRNA for (epsilon) chain of rat immunoglobulin E."; Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).
                                                                                                                                                                                                                                   SEQUENCE OF 168-342 FROM N.A. (MY MEDLINE=83182019; PubMed=6820340;
                                                                                                                                                                                                                                                                                                                                          STRAIN=LOU/C/WSL;
MEDLINE=83064537; PubMed=6292865;
              This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                    "A cloned cDNA probe for rat construction, identification,
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Mammalia, Eutheria,
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Pfam; PF00047; ig; 4.
SMART; SM00407; IGcl; 1.
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PR0SITE; PS00290; IG_MHC; 3.
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MEDLINE=84088930; PubMed=6418803;
MEDRINE=14088930; PubMed=6418803;
MEDRINE=14088930; PubMed=6418803;

"Complete sequence of a cloned cDNA encoding rabbit sec of VHa2 allorype: comparisons with VHa1 and membrane muj. Immunol. 132:490-495(1984).

-i- ALTERNATIVE PRODUCTS:
                                                                                                                                     20-MAR-1987 (Rel. 04, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g mu chain C region membrane-bound form.
0ryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its modified and this statement is not removed. Usage entitles requires a licemen security.
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PIR; A93442; EHRT
HSSP; P01854; 1IG
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Event=Alternative splicing; Named isoforms=2.
Comment=During differentiation, B lymphocy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                          QNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
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"Amino acid sequence of the Fc region of a canine interspecies homology for the IgM class.";
Science 200:1159-1161(1978).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCumber L.J., Capra J.D.;
"The complete amino-acid sequence
Mol. Immunol. 16:565-570(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora;
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Canis familiaris (Dog).
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TNEVZAZAKZSGPTTYKVTSMLTIQEDAWLSQSVFTCKVEHRGLTFQQNASSM---
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DOMAIN
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                        "The primary structure of mu-chain-disease protein BOT. amino-acid sequence of the N-terminal 42 positions."; Hoppe-Seyler's Z. Physiol. Chem. 365:105-118(1984).
-!- MISCELLANEOUS: This protein has no V region homology
                                                                                                                                                                                                  Immunoglobulin
DOMAIN 1
                                                                                                                                                                                                                                                                                                                            GO; GO:0005624;
GO; GO:0003823;
                                                                                                                                                                                                                                                                                                                                                      PIR; A02163; MHHUBT.
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=84184186; PubMed=6425189;
Barnikol-Watanabe S., Mihaesco E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-MAR-1987 (Rel. 04, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Ig mu heavy chain disease protein (BOT).
                                                                                                                                                                                                                                                                       30; GO:0006955; P:immune response;
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hilschmann N.;
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                        157
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                                                18
                                                                                                             Similarity
KLICQATGFSPRQIEVSWLREGKQVGSGVTTDEVEAEAKESGPTTYKVTSTLTIKESDWL 128
                       -----SPR-----
                                                 EAEDRIIKEEEARL----
                                                                       EVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWTREENGALKTHTNISESHPNGTFSAMGEATVCVEEWESGEQFTCTVTHTDLPSVLKQT
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391
                                                                                                 Conservative
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                                                                                                                                               STANDARD;
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                                                                                                            13.5%;
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                                                                                                 65;
                                                                                                                                                                                                                                                                                                                             fraction; NAS pinding; TAS.
                                                                                               Score 365.5; DB 1;
Pred. No. 2.3e-16;
5; Mismatches 132;
                                                -SGRD----MQVTSQPVIAELPPKVSVFVPPRDGFFGNPRKS
                      -ĠKNIQGGKŢLSVSQLĒLQDSG----ŢWŢCŢVLQN---
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RESULT 41
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MEDLINE=82051295; PubMed=6795090;
Goldberg G.I., Vanin E.F., Zrolka A.M.,
"Sequence of the gene for the constant;
"Sequence immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDIJINE=81076590; PubMed=6255422;
MEDIJINE=81076590; PubMed=6255422;
Kawakami T., Takahashi N., Honjo T.;
Kawakami T., Takahashi N., Honjo T.;
"Complete nucleotide sequence of mouse immunoglobulin comparison with other immunoglobulin heavy chain genes Nucleic Acids Res. 8:3933-3945(1980).
                                                                                                [5]
REVISION (MOPC 104E).
MEDLINE-83075344; PubMed-6816276;
MEDLINE-83075344; PubMed-6816276;
                                                                                                                                                          SEQUENCE (MYELOMA PROTEIN MOPC 104E).

MEDLINE=79223904; PubMed=111247;

MEDLY M.R., Sibley C.H., Fuhrman J.S., Schilling

"Amino acid sequence of a mouse immunoglobulin m

"Amino acid sequence of a mouse immunoglobulin m

"Proc. Natl. Acad. Sci. U.S.A. 76:2932-2936(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig mu chain C region secreted form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                       heavy chain constant region domains Biochemistry 21:5415-5424(1982).
-i- SUBCELLULAR LOCATION: Secreted-
-i- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P01872;
                                                                                                                                                                                                                                                                                   Auffray C.,
                                                                                           Kehry M.R., Fuhrman Hood L.E.;
                                                                                                                                                                                                                                                                                                                                       Gene 15:33-42(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                'Complete amino acid sequence
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               Event-Alternative
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12:77-86(1980)
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Rodentia;
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aplicing; Named isoforms=2;
differentiation, B lymphocytes
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                                                                domains.";
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Sciurognathi;
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chi; Muridae; Murinae; Mus.
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG LIKE;
PROSITE; PS00290; IG MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; V00827; -; 1
PIR; A02166; MHMS
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IsoId=P01872-1; Sequence=Displayed;
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178
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                                                                                                                                                                                                                                                                                           Similarity
YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST---
                            ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                SPP----GSSP---SVQCR----SPR-----GKNIQGG-----
                                                                                                                                    TSQVLLSPKSILEGSDEYLVCKIH-----YG-GKNRDLHVPIPAVAEMNPNVNVF
                                                                                                                                                                 ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE
                                                                                                                                                                                                     VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT------
                                                                VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                                                                                                                                       VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splicing.
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                                                                                                                                                                                                                                                                         84;
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Pred. No. 4.6e
34; Mismatches
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N-LINKED
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C-TERMINAL
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BY SIMILARITY.
INTERCHAIN (WITH
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S--N (IN MOPC 1045).
H->Q (IN MOPC 1045).
T--N (IN TEPC183 AND M
N--> T (IN MOPC 1045).
N--> S (IN TEPC183).
L--> K (IN TEPC183 AND M
4CBE57CB602F9B51 CRC64
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(GLCNAC...)
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                                                                                                                                                                                                                                                          MEDLINE=84236029; PubMed=6234164;
Flanagan J.G., Rabbitts T.H.;
"The sequence of a human immunoglobulin epsilon
region gene, and evidence for three non-allelic
EMBO J. 1:655-660(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=83168897; PubMed=6300763; Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Kikuchi M., Sugino Y., Nishida Y., Honjo T.; "Molecular cloning and nucleotide sequencing of huepsilon chain cDNA.";
 "Cloning and sequence determination of the gene for immunoglobulin epsilon chain expressed in a myeloma Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                              SEQUENCE OF 1.40; 68-114 AND 427-428
MEDLINE=83065224; PubMed=6815655;
Kenten J.H., Molgaard H.V., Houghton
Bell L.O., Gould H.J.;
                                                                                                                                         PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=83001945; PubMed=6288268;
Max E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
"Duplication and deletion in the human immunoglobulin epsilon
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ch M.K. (eds.);
ste hypersensitivity: modern c
new York (1978).
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1:1539-1544(1982).
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GO; GO:0003823; F:antigen bin GO; GO:0006955; P:immune resp. InterPro; IPR007110; Ig-like. InterPro; IPR003597; Ig C1. InterPro; IPR003597; Ig C1. InterPro; IPR003006; Ig_MHC. Pfam; PF00047; Ig; 4. SMART; SM00407; IGC1; 4. PROSITE; PS00835; IG LIKE; 4. PROSITE; PS00835; IG MHC; 3.
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Manual of the Fc of immunoglobulin
Mal. Immunol. 23:1063-1075(1986).
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Oryctolagus cuniculus (Rabbit).
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3; Mismatches 137;
  Craniata;
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MEDLINE=84088930; PubMed=6418803;
Bernstein K.E., Alexander C.B., Redd
"Complete sequence of a cloned cDNA."
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InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           venteAlternative splicing; Named isoforms=2;
Comment=During differentiation, B lymphocytes switch from comment=Ouring differentiation, B lymphocytes switch from comments of isoform Membrane-bound to isoform Secreted;
                      51
                                             77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P03988-1; Sequence=Displayed;
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 00047; ig; 4.
M00407; IGc1; 2.
PS50835; IG_LIKE; 4
PS00290; IG_MHC; 3.
VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR---
                                             NDRADSRRSLWDQGNFPLIIKNLK----
                                                                     ALTDGNLVAMG-----CLARDFLPSSVTFSWSFKNNSEI------
                                                                                          AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria; Lagomorpha; Leporidae; Oryctolagus
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                                                                                                                                                                                                                                                                                                                                                                                                        splicing
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                      -SSRTV---RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR
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cDNA encoding rabbit secreted mu-chain
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                                                            PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immuno
                                                                                                 InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR00306; Ig_MHC.
Pfam; PP00047; Ig; 4.
SMART; SM00407; IGc1; 3.
                                                                                                                                                                             EMBL; X13920; CAA32113.1; ALT_INIT.
PIR; S03961; S03961.
                                                                                                                                                                                                                                                                                                                        MEDLINE=89232144; PubMed=2497033; Ishiguro H., Ichihara Y., Namikawa T., "Nucleotide sequence of Suncus murinus comparison with mouse and human mu gene FEBS Lett. 247:317-322(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Veri
Mammalia; Eutheria; Insectivora; Soricidae;
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Suncus murinus (House shrew) (Musk shrew).
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01-FEB-1991 (Rel. 17, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Liver;
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dae; Crocidurinae; Suncus.
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HYVTSNPTPEPQNPGLYFVHSILTVSEKDWSSGESFSCVVGHEALPLSVTEKAVDKTSG
                                                                             QSLSRPKDVANDPPSVFVLPPAQEQLKLRESASITCLVKDFSPPD
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                                                                                                                   KTISKAKGQPRE-PQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGOP--EN
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Conservative 7:
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INTERCHAIN (WITH HEAVY BY SIMILARITY.

INTERCHAIN (GLCNAC...)

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Pred. No. 1.4e-15;
1; Mismatches 163;
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P06337;
01-Jan
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01-FEB-1996
15-JUL-1999
SEQUENCE FROM N.A.

MEDLINE-85297761; PubMed=2994005;

MCGuire K.L., Duncan W.R., Tucker P.W.;

"Phylogenetic conservation of immunoglobulin comparison of hamster and mouse Cmu genes.";

Nucleic Acids Res. 13:5611-5628(1985).
                                                                                                                                                            Mesocricetus auratus (Golden hamster)
Eukaryota; Metazoa; Chordata; Craniat
Mammalia; Eutheria; Rodentia; Sciurog
                                                                                                                        Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                 01-JAN-1988 (Rel. 06, Created)
01-FEB-1996 (Rel. 33, Last seq
15-JUL-1999 (Rel. 38, Last ann
                                                                                                                                                                                                                                                                                                               MESAU
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annotation update)
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            LPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGS--FF
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IPR003597;
QPLAREQLILRESATVTCLVKGFSPADIFVQWLQRGQPLSQDKYVTSAPMREPQAPHLYF
                                                              YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYT
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llarity 24.9%;
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Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Ria Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Rian Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Rian Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Rian Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Rian Hopkins R.F., Jordan H., Moore T., Max S.I., Wang L.,

Rian Hopkins R.F., Jordan R., Foshiyuki S., Carninci P., Prange C.,

Rian Hopkins R.F., Jordan N., Poters G.J., Abramson R.D., Mullahy S.J.,

Rian S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Schernan N.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Schergren B.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Schergren B.J., Lu X., Gibbs R.A.,

Richards S., Wadan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rahesjley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rochnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

Thuman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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P09564;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
T-cell antigen CD7 precursor (GP40) (T-cell leukemia
Haynes B.F.;
"Characterization of th
                                                       Ware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schanberg L.E., Fleenor D.E., Kurtzberg J., Haynes I "Isolation and characterization of the genomic human structural similarity with the murine Thy-1.gene."; Proc. Natl. Acad. Sci. U.S.A. 88:603-607(1991).
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                                                                                                                                                                     Takahashi T.;
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Mammalia;
                                                                        MEDLINE=90063052;
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"Molecular cloning of two
                                                                                                                                        differentiation
                                                                                                                                                                                      Yoshikawa
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6:3313-3316(1987).
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n antigen CD7.";
33:352-360(1991)
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                                                     PubMed=2479685;
e R.M., Dietz M.A.,
      of the surface topography numan CD7 molecule.";
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EMBL; D00747; BAA00646.1; JOINED.
EMBL; D00748; BAA00646.1; JOINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0016021; C:integral to membrane; TJ GO:0016024; C:membrane fraction; TAS. GO:0005886; C:plasma membrane; TAS. GO:0004872; F:receptor activity; TAS. GO:0004952; P:immune response; TAS. GO:0004910; P:f. cell activation; TAS. GO:0004210; P:f. cell activation; TAS. GO:0007169; P:transmembrane receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 1 immunoglobulin-like domain. DATABASE: NAME=PROW; NOTE=CD guide CD7 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd7.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: Interacts with
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                    321 ISKAKGOP---
                                                             Similarity
90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g requires a license agreement (See http://www.isb-sib.ch/announce,
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal;
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162
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180
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240
-----REPQVYTLPPSRDEL:fXNQVSLTCL----VKGFY------PS 360
                                                                                                                                            25409 MW;
                                                                                  11.7%;
41.7%;
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Receptor;
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                                                                                  Score 316.5;
Pred. No. 1.0
                                                                                                                                                                                                                                       S-palmitoyl cysteine.
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
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                                                                                                                                                                                                                                                                                                                                                                                     IG-LIKE
                                                                                                                                          EBBCE08279552108 CRC64;
                                                         ed. No. 1.6e-13;
Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor protein tyrosine kin. . .; NAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; Transmembrane; Lipoprotein; Palmitate;
                                                                                                                                                                                                                                                                                                                                                                 AA TANDEM REPEATS, POTENTIAL SPACER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the human K12 (SECTM1)
                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (PROBABLE)
                                                                                                   Length
                                                                                                   240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat
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RESULT 47
HVC2_HETFR
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Query Match
Best Local Similarity
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DOMAIN
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Ig heavy chain C region (Clone 12022) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes;
Heterodontidae; Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HVC2_HETFR P23085;
                                                                                                                                                                                                                   SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the ENthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                            Immunoglobulin
                                                                                                                                                                                                                                                                                                                             EMBL; X07784; CAA30617.1; -.
                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman G.W.; "Complete structure and organization of immunoglobulin heavy chain constant region genes in a phylogenetically primitive vertebrate.", EMBO J. 7:1979-1988 (1988).

-i- SIMILARITY: Contains 4 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991
01-NOV-1991
                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                  InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                       HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                 PIR; S00980; HVRKC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88328985; PubMed=3138109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7792;
                                                                                                                                                                                                                                                       Pfam; PF00047; ig;
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                                   1108
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AA;
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42, Last annotation update)
region (Clone 12022) (Fragment).
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202
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Ig_cl.
Ig_MHC.
                                    47904
11.5%;
25.4%;
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                                    MW;
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Pred.
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IG-LIKE
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 312; DB 1;
No. 6.8e-13;
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                                    CRC64;
           Length 438;
                                              (POTENTIAL).
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21-JUL-1986
01-FEB-1991
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                    Weill J.-
                                                                            EMBL; X01613; CAA25762.1;
PIR; A02170; MHCH.
                                                                                                                                                      the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAR-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 80-446 FROM N.A. MEDIJINE-83299221; PubMed-6311496; Dahan A., Reynaud C.-A., Weill J.-C.; "Nucleotide sequence of the constant richain immunoglobulin mRNA."; Nucleic Acids Res. 11:5381-5389(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig mu chain C region.
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
  HSSP; P01857; 1FC1.
InterPro; IPR007110;
InterPro; IPR003597;
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PROSITE; PS00290; IG_MHC;
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SMART; SM00407; IG
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                                                                              TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVYTLPPSRDE
                                                                                                    DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                 LINGNORLSVICMAQGENEPHLEVRWWRNGEPLPQSQSVTSAPMAENPENESYVAYSVLGV
                                            LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDS--DGSFFLYSKLTV
                                                                    LYTVDGVATVCASEWDGGDGYVCKVNHPDLLFPMEEKMRKTKASNARPPSVYVFPPPTEQ
                                                                                                                                          RISVTESEWDTGATFSCVV-----
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                                                                                                                                                          TLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC---PELLGGPS
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(BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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Pred. No. 8.7e-13;
7; Mismatches 179
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RESULT 49
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ID HVCM HETFR STANDARD;
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SMART; SM00407; IGc1; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentaties requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONSTANT region genes in a EMBO J. 7:1979-1988(1988).
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NCBI_TaxID=7792;
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Heterodontus francisci (Horn shark)
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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ROSITE; PS00290; IG_MHC; 3.
mmunoglobulin_domain;_Immunoglobulin_C region; Glycoprotein;
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  SRNITGSQVPC----
                                      KIDI-----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                                                                    -----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF
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Pred. No. 3.4
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                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                  SEQUENCE (MYELOMA PROTEIN LAN).
MEDLINE=79180140; PubMed=286295;
Tsuzukida Y., Wang C.-C., Purnam F.W.;
"Structure of the A2m(1) allotype of human IgA --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flanagan J.G., Lefranc M.-P., Rabbitts T.H.; "Mechanisms of divergence and convergence of the human alpha 2 constant region gene sequences."; Cell 36:681-688(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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15-MAR-2004
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                                                                                                                                                                                                                                                                                REVIEW
                                                                                                                                                                                                                                                                                                                        molecule
                                                                                                                                                                                                                                                                                                                                                                                                      "Complete amino acid sequence of the alpha 2 heavy IgA2 immunoglobulin of the A2m (2) allotype."; Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Torano A., Putnam
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=78137069; PubMed=416441;
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MEDLINE=84130179; PubMed=6421489;
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                                                                                                                                                                                                                     "The structure and function of human slochem. J. 271:285-296(1990).
                                                                                                                                                                                                                                                     Kerr M.A.;
                                                                                                                                                                                                                                                                                                         Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [g alpha-2 chain
                                                                                                                 SUBUNIT: Monomeric or polymeric.
MISCELLANEOUS: The sequence of the A2m(1) allotype is shown
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                            FUNCTION: Ig alpha is the major immunoglobulin class in secretions. It may serve both to defend against local in and to prevent access of foreign antigens to the general
                                                                                                                                                                immunologic system
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SMART; SM00407; IGcl; 2.
PROSITE; PS50835; IG_LIKE; 3
PROSITE; PS00290; IG_MHC; 2.
Immunoglobulin domain; Immun
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MIM, 147000; -.
GO; GO:0005624; C:membrane
GO; GO:0003823; F:antigen b
GO; GO:0006955; P:immune re
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                                                                                                                                                                              Similarity
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                                          STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                              PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                   TTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---DVTVPCPVPPPPPPC----
                                                                                                               LSVSQLEL----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                    VFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDASGDLY
LALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILR
                LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLT
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IPR003597; Ig_cl.
IPR003006; Ig_MHC.
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P:immune response;
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P-> S (IN A2M(2) ALLOTYPE).
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Pred. No. 6.5e-12;
0; Mismatches 143
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/FTId=VAR_003883.
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F -> Y (IN A2M(2) ALLCTYPE)
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D -> E (IN A2M(2) ALLCTYPE)
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between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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Kokubu F., Hinds K., Litman K., Shamblott M.J., Litman G.W.;
Kokubu F., Hinds K., Litman K., Shamblott m.J., Litman G.W.;
"Complete structure and organization of immunoglobulin heavy chain
constant region genes in a phylogenetically primitive vertebrate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Heterodontoidea; Heterodontiformes; Heterodontidae; Heterodontus.
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01-NOV-1991 (Rel. 20, Last sequence upd
15-JUL-1999 (Rel. 38, Last annotation u
Ig heavy chain C region, secreted form
Heterodontus francisci (Horn shark).
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SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG LIKE; 4
PROSITE; PS00290; IG_MHC; 3.
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PIR; S01853; HVRKCS.
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IPR003006; Ig_MHC.
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              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003596; Ig_MHC.
Pfam; PF00047; Ig; 2.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RABIT
                                                                                                                                      EMBL; X00353; CAA25100.1; -. PIR; A02174; AHRB.
                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                Knight K.L., Martens C.L., Stoklosa C.M., Schneiderman R. "Genes encoding alpha-heavy chains of rabbit IgA: charact cDNA encoding IgA-g subclass alpha-chains.";
Nucleic Acids Res. 12:1657-1670(1984).

-i- FUNCTION: Ig alpha is the major immunoglobulin class secretions. It may serve both to defend against local and to prevent access of foreign antigens to the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALC RABIT STANDARD; PRT; 299 AA P01879; PRT; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation updat Ig alpha chain C region (Fragment).
                                                                                                                                                                                                                                                                              This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9986;
                                                                                                                        HSSP; P01857; 1FC1.
   mmunoglobulin
                                                                                                                                                                                                                                                                                                   It was isolated from a rabbit homozygous FOR A2, N8 F71, G75 heavy chain haplotype.
SIMILARITY: Contains 2 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                   immunologic system.
MISCELLANEOUS: This immunoglobulin belongs to the IgA-G
                                                                                                                                                                                                                                               European
                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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RESULT 53
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions
                                                                    Pfam; PF00047; ig; 3.

SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                              PIR; S01851; HVRKC5.
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as modified and this statement is not rementities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   constant region genes in a phylogenetically primitive EMBO J. 7:1979-1988(1988).
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                                                                                                                                                                    InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                              EMBL; X07783; CAA30616.1;
                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 3 immunoglobulin-like domains
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(Rel. 20, Last sequence update)
(Rel. 42, Last annotation update)
ain C region (Clone 6125) (Fragment).
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Pred. No. 6.9e-12;
2; Mismatches 106
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IG-LIKE 2.
2512FE3F62E9A223
  IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Chondrichthyes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370
                                                                                                                                                                                                                                                                                                                                                                     (See
                                                region; Glycoprotein; Repeat
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                                                                                                                                                                                                                                                                                                                                                                                                              its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
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Best Local S
Matches 101
                                                                                                                                                                                                                                   HVC3 HETFR STANDARD; PRT; 393 AA.

P23086;
01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 heavy chain C region (Clone 6121) (Fragment).
Heterodontus francisci (Horn shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Elasmobranchi; Galeomorphi; Heterodontoidea; Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                       JLT 54
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DOMAIN
CARBOHYD
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SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMEL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                  MEDLINE=88328985; PubMed=3138109; Kokubu F., Hinds K., Litman R., Shamblott M.J., Litman "Complete structure and organization of immunoglobulin constant region genes in a phylogenetically primitive v EMBO J. 7:1979-1988(1988).
                                                                                                     -MBO J. 7:1979-1988(1988).
-M- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=7792;
                                                                                                                                                                                     SSUE=Spleen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK-AKGQPREPQVYTLPPSRDELTKNQ-V
                                                                                                                                                                                                                                                                                                                                                                                                                          ASYSCVVGHEAI PLKI I NRTVNKSSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-LEATVTLTCV---VSNAPYGVNVSW-----TQEQKPLKSEIAVQPGEDPDSVIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY-----NSTYRVVSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VQLLVFGLTAN--SDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSKIYCEVRRGESLWIKEIPDCKGDIVHPTVILTQTSSEEITSSRFATVVCSIIDFHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPSKLNDRADSRRSLW-----DQGNFPLIIKNLKIEDSD----TYICEVEDQKEE
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IG-LIKE 3
N-LINKED
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Pred.
                                                                                                                                                                                                                                                 Heterodontoidea; Heterodontiformes;
                                                                                                                                                                                                                                                               Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ore 286.5; DB 1; ed. No. 2.3e-11; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                          351
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(POTENTIAL).
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in heavy chain
e vertebrate.";
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               ch/announce/
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Ig alpha-1 IGHA1.

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(Rel. (Rel. (Rel.

17, Creat 17, Last 42, Last region.

sequence

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update)

Created)

STANDARD;

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gorilla gorilla

(Lowland

gorilla)

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RESULT
ALC1_GC
ID ALC
AC P2
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Best Local
                          11. GORGO
ALC1 GORGO
P20758;
01-FEB-1991
01-FEB-1991
10-OCT-2003
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CARBOHYD
SEQUENCE
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NON TER 1
DOMAIN 63
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG LIKE;
PROSITE; PS00290; IG MHC; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X07782; CAA306; PIR; S01852; HVRKC1. HSSP; P01842; 7FAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQGNKV---VLGKKG----DTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKL
                                                                                                                                       LHNHYTQKSLSLSPG
                                                                                                                                                                                                                         KEYKCKVSNKALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVSLTCLVKGFYP
                                                                                                                                                                                                                                                       VTLNCI---VSNAPYGVNVSW---TQEQKSLKSEIAVQPGEDADSVISTVNISTQAWLSG
                                                                                                                                                                                                                                                                                                                       VLQNQKKVEFKIDI----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRT
                                                                                                                                                                                                                                                                                                                                             -PESITVSWLKDGQHMESGFVTSPT--C---
                                                                                                                                                                                                                                                                                                                                                                QGQSLTLT-----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCT
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                                                                                                                             IPLKIINRTVNKSSG
                                                                                                                                                                      REIFVKWTINDKSVNPGNYKNTEVMAENDNSSYFIYSLLSIAAEEWASGASYSCVVGHEA
                                                                                                                                                                                         SDIAVEWESNGOPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEA
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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No. 5.7e-11;
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b (GLCNAC. ...
c (GLCNAC. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 393,
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kawamura S., Omoto K., Ueda S.;
"Nucleotide sequence of the gorilla immunoglobulin alpha 1 gene.";
Nucleic Acids Res. 17:6732-6732(1989).
-!- FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infectio and to prevent access of foreign antigens to the general
                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pf4m; PF00047; ig; 3.
SMART; SM00407; iGc1; 2.
PROSITE; PS50835; iG LIKE; 3.
PROSITE; PS00290; iG_MHC; 1.
                                                                                                                                                                                                                                                                                   DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15045;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89386006; PubMed=2506527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunologic system.
SIMILARITY: Contains 3 immunoglobulin-like domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produsen the Swiss Institute of Bioinformatics
293
                      135
                                           233
                                                                                        187
                                                                                                                                     127
                                                                 88
                                                                                                              59
                                                                                                                                                                     Similarity
                                                                                        LQNQKKVEFKIDIVPC----
VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLT
                      ED-LLLGSEANLTCTLTGL-RDASGVTFTWTPSSGK--SAVEGPPERDLCGCYSVSSVLP
                                          KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLT
                                                                                                                                  ANSDITHLIQGOSLITLILESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTV
                                                                 -- NHYTNPSQDVTVPCRVPSTPPTPSPSTPPTPSPPCCH-
                                                                                                              ASGDLYTTSSQ---LTL-----PATQC--PDGKSV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR007110; Ig-like.
IPR003597; Ig_cl.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria;
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353 AA;
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                                                                                                                                                          Conservative
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147
182
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122
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                                                                                                                                                                    10.3%;
28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin C region; Glycoprotein; Repeat.
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BY SIMILARITY.
INTERCHAIN (WITH )
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
SIMILARITY).
                                                                                                                                                                   Score
Pred.
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                                                                                                                                                                                                                                       SIMILARITY)
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                                                                                                                                                                                                                                                                        SUBUNIT)
                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH HEAVY CHAIN)
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BY SIMILARITY
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                                                                                                                                                                                                                                                INTERCHAIN (WITH J CHAIN)
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                                                                                        -----PAPEPKSCDKTHTCPELLGGPSVFLFPPKP
                                                                                                                                                          Mismatches
                                                                                                                                                                    279;
No. 6.
                                                                                                                                                                                                                                                                      (BY SIMILARITY).
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MBL outstation -
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Yang C.-Y., Kratzin H., Gotz H., Hilschmann N.;
"Rule of antibody structure. Primary structure of a h
"ga-immunoglobulin (myeloma protein Tro). VII. Purifi
characterization of the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 360:1919-1940(1979).
          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                  immunologic system.
-!- SUBUNIT: Monomeric or polymeric.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                    "The primary structure of a monoclonal IgA-immunoglobulin II. The amino acid sequence of the H-chain, alpha-type, su structure of the complete IgA-molecule.";
Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel.
01-FEB-1991 (Rel.
15-MAR-2004 (Rel.
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                                                                                                                                            Biochem. J.
                                                                                                                                                                                                                                                                                                                           DISULFIDE BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE (MYELOMA PROTEIN TRO).
MEDLINE=76023781; PubMed=809331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putnam F.W., Liu Y.-S.V., Low "Primary structure of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flanagan J.G., Lefranc M.-P., Rabbitts T.H.; Mechanisms of divergence and convergence of the huma alpha 2 constant region gene sequences."; Cell 36:681-688(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=84130179;
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Mammalia; Eutheria;
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                                                                                                                                                                             Kerr M.A.;
                                                                                                                                                                                      MEDLINE-91054387; PubMed-2241915;
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[5]
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amino acid sequence of the alpha 1 heavy
7. Biol. Chem. 254:2865-2874(1979).
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                                                                                              FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infect and to prevent access of foreign antigens to the general
European
                                                                                                                                                            structure and function of human
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                                                                                                                                               271:285-296(1990)
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Bioinformatics
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43, Last
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(See http://www.isb-sib.ch/announce/

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MIM, 146900; -.

GO; GO:0003923; F:antigen binding; NAS.

QO; GO:0003955; P:immune response; NAS.

R InterPro; IPR007110; Ig-11ke.

R InterPro; IPR003597; Ig_C1.

R InterPro; IPR003597; Ig_C1.

NR Pfam; PF00047; Ig; 3.

DR PMART; SM00407; IGC1; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS50835; IG_MIC; 1.

R Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

RMM Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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PDB; 1IGA; 15-JUN-
                                                                                                                                                                                                                                                                  SEQUENCE
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                        253
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RDASGVTFTWTPSSGK--SAVQGPPERDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPE
                       HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
                                                                                                                              QSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFK 196
                                                                           IDI-VECEAPEPKSCDKTHTCPELLGG---PSVFLFPPKPKDTLMISRTPEVTCVVVDVS
                                                                                                                                                                                  FPLIIKNLKIEDSDTYICEVEDQKEEVQLLVF-----GLT-----ANSDTHLLQG
                                                                                                                                                          FPLSLCSTQPDGNVVIACLVQGFFPQEPLSVTWSESGQGVTARNFPPSQDASGDLYTTSS
                                                    -DVTVPCPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALED-LLLGSEANLTCTLTGL-
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N-LINKED (GLCNAC...).

E -> D (in dbSNP:1407).

/FTId=VAR 014602.

TPS -> PST (IN REF. 2).

E -> B (IN REF. 3).

P -> S (IN REF. 3).

R -> H (IN REF. 3).

H -> R (IN REF. 3).

H -> R (IN REF. 3).
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Pred. No. 8.3e-
51; Mismatches
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O-LINKED.
O-LINKED.
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IG-LIKE 2.
IG-LIKE 3.
INTERCHAIN
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INTERCHAIN (WITH HEAVY CHAIN OF
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OR 123-182
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes; Ictaluridae; Ictalurus.
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MEDLINE=90384824; PubMed=2119496;
MEDLINE=90384824; PubMed=2119496;
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Ig mu chain C region membrane-bound
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Mammalia; Eutheria; Rodentia;
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Immunoglobulin (
NON TER 1
DOMĀIN 6
DOMAIN 116
 VARIANT
VARIANT
SEQUENCE
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PIR; A91479;
HSSP; P01810;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general immunologic system.

-!- MISCELLANEOUS: The final C-region domain is deleted from Ref.2 chain. It was isolated from a myeloma protein that contains 1 light and 1 heavy chain per molecule, linked by a disulfide bond. In contrast, normal mouse IgA molecules contain 2 light and 2 heavy chains and lack a light-heavy chain disulfide bond. heavy chains and lack a light-heavy chain disulfide bond.
-!- MISCELLANEOUS: M511 chain was isolated from a myeloma protein that binds phosphorylcholine.
-!- MISCELLANEOUS: M511 sequence was compared with that of mouse MOPC 47A, and a genetic mechanism for the deletion of the CH3 domain of the mutant chain is proposed.
                                                                                                                                                                                                         VARIANT
VARIANT
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 2
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                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                   CARBOHYD
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InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete amino acid sequence of a mouse immunoglobulin alpha (MOPC 511).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robinson E.A., Appella E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01810;
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domain;
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Ig_cl.
! Ig_MHC.
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IG-LIKE 3.
IG-LIKE 3.
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Query

Match

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Score 264.5;

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RESULT 59
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AC STALIN
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Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-regulatory protein alpha-1) (Sirp-alpha-1) (mSIRP-alpha-1) (MyD-1 antigen) (Brain Ig-like molecule with tyrosine-based activation motifs) (Bit) (p84).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHS1_MOUSE (
P97797; O08907;
Q9WTN4;
                                                                SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SEQUEN (ISOFORM 2), VARIANTS ALA-29; ARG-91; THR-96 N-GLYCOSYLATION, AND TISSUE SPECIFICITY.
STRAIN-BALB/C; TISSUE-Brain, and Cerebellum; MEDLINE-98012243; PubMed-9348339; Comu S., Weng W., Ollnsky S., Ishwad P., Mi 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamao T., Matozaki T., Amano K., Matsuda Y., Takahas Fujioka Y., Kasuga M., "Mouse and human SHPS-1: molecular cloning of cDNAs localization of genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                       Lagenaur C.F., Narayanan V.; "The murine P84 neural adhesion molecule
                                                                                                                                                                                                                                                                                               Ohnishi
                                                                                                                                                                                                                                                                                                                         MEDLINE=97230468; PubMed=9073522;
                                                                                                                                                                                                                                                                                                                                                  STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97223399; PubMed=9070220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                              H., Kubota M., Sano S.-I.; it) maps to mouse chromosome s 40:504-506(1997).
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                                                                                                                                                                                                                                                                                                                                                                          PRO-194 AND
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                       ASN-224.
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Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 231:61-67(1997).
                                                                                                                                                                                                                                                                                                                                                                                              AND VARIANTS ALA-29; ARG-67; ARG-91,
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                                                                                                                                                                                                SEQUENCE OF 32-53
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thi; Muridae;
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                         SHPS-1,
                                                                                                                                                                            AND
                                                                          Hempel
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Murinae; Mus
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MEDLINE=20130295; PubMed=10662797;
Gresham H.D., 'Dale B.M., Potter J.W., Chang P.W., Vines C.M.,
Lowell C.A., Lagenaur C.F., Willman C.L.;
"Negative regulation of phagocytosis in murine macrophages by the
kinase family member, Egr.";
J. Exp. Med. 191:515-528 (2000).
-!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), VARIANTS ALA-29; ARG-67; PRO-74; ALA-83; 86-TYR VAL-87; ILE-90; ARG-91; THR-96; ALA-114; ILE-91; ASR-128; PRO-194; ASN-224; PHE-351 AND ASP-365; N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, INTERACT WITH EPFN6, AND TISSUE-FECAL CHYONUS; STRAIN-C57BL/6; TISSUE-FECAL CHYONUS; MEDLINE-98380500; PubMed-9712903;
                                                                                                                                                                         MEDLINE-99091586; PubMed-9872987
Jiang P., Lagenaur C.F., Narayan
"Integrin_associated protein is
                                                                                                                                                                                                                                                              Stofega M.R., Wang H., Ulli
"Growth hormone regulation
and association.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehringer M.A., Thompson J., Conroy O., Xu
Beeson M., Gordon L., Bennett B., Johnson
"High-throughput sequence identification
"Within alcohol-related QTLs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO-74; ALA-83; 86-T
ILE-118; SER-128; PR
STRAIN=ILS, and ISS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/SvJ, and C57BL/6; TISSUE=Br MEDLINE=20053880; PubMed=10588853; Sano S.-I., Ohnishi H., Kubota M.; "Gene structure of mouse BIT/SHPS-1."; Biochem. J. 344:667-675(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Neurosci. 17:8702-8710(1997) [4]
                                                                                                      INTERACTION WITH FGR. MEDLINE=20130295; Put
                                                                                                                                                                                                     INTERACTION WITH CD47, AND TISSUE SPECIFICITY MEDLINE-99091586; PubMed-9872987;
                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION, TISSUE SPECIFICITY, AND MEDLINE=90152134; PubMed=2303162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang H., Chen Z.,
"Epidermal growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-GLYCOSYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Veillette A. Thibaudeau E., Latour S., "High expression of inhibitory receptor with protein tyrosine phosphatase SHP-1 J. Biol. Chem. 273:22719-22728(1998).
                                                                                                                                                               molecule.
                                                                                                                                                                                                                                                                                                                                                                                  neurite outgrowth
                                                                                                                                                                                                                                                                                                                                                                                                              Chuang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
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                                                                                                                                                                                                                                                                                                            MEDLINE=98175985; PubMed=9507023;
                                                                                                                                                                                                                                                                                                                          HORMONE,
                                                                                                                                                                                                                                                                                                                                                                                              Chuang W., Lagenaur C.F. "Central nervous system
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                                                                                                                                                                                                                                                                                                                       GLYCOSYLATION, PHOSPHORYLATION BY PROONE, AND INTERACTIONS WITH JAK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome 12:657-663 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JAN-1997)
                                                                                                                                                                                                                                                                                                                                                                  137:219-232(1990)
                                                                                                                                                 274:559-562(1999).
                                                                                                                                                                                                                                                   273:7112-7117(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .A. (ISOFORM 2), AND VARIANTS ALA-29; ARG-67; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-18; PRO-194; ASN-224; PHE-351 AND ASP-365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor-induced association of SHP2 with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ullrich A.;
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                                                                                                                                                                         Narayanan V.;
tein is a ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                             Carter-Su C.;
and SHP-2 tyrosyl
                                                                                                                                                                                                                                                                                                                                                                                               can
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AND PTPN11.
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., Sikela J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liver;
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                                                                                                                                                                            neural adhesion
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IsoId=P97797-3; Sequence=VSP_007031;

-:- TISSUE SPECIFICITY: Highly expressed in cerebral cortex, brain, spinal cord, cerebellum and spleen, and at much lower levels in kidney, thymus, heart, lung and liver. Within the cerebellum, highly expressed throughout the molecular layer, and in synaptic glomeruli in the granule cell layer. Detected in neurons of the hippocampus and dentate gyrus, and in olfactory bulb. Not detected in Purkinje cells. Highly expressed in the plexiform layers, optic fiber layer and the outer segments of the photoreceptor layer in the retina. Highly expressed in macrophages. Isoform 3 is detected at very low levels in all tissues tested.

--- DEVELOPMENTAL STAGE: Highly expressed in the CNS of embryos from day 7 to 17.
                                                                                                                                                  EMBL;
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PTM: Phosphorylated on tyrosine residues.

SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.

SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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IsoId=P97797-1; Sequence=Displayed;
Name=2; Synonyms=a', Large;
IsoId=P97797-2; Sequence=VSP_007032;
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ALTERNATIVE PRODUCTS:
AF072543; AAC24886.1; AF072544; AAC24887.1; AF072544; AAC24887.1; AB024507; BAA89290.1; JOIN AB024501; BAA89289.1; JOIN AB024501;
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Best Local
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MGD; MGI:108563; Ptpns1.

GO; GO:0008580; F:cyttoskeletal regulator activity; IMP.
GO; GO:0045309; F:phosphoprotein amino acid binding; IPI
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007015; P:actin filament organization; IMP.
GO; GO:0007150; P:cell motility; IMP.
GO; GO:0007160; P:cell-matrix adhesion; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF332079; AAK56107.1;
EMBL; AF332080; AAK56108.1;
EMBL; Y10349; CAA71375.1;
                                                                                           424
                                                                                                                        291
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                                                                                                                                                                                     HITLDR--SPLEGIANLSNFIRVSPTVKVTQQSPTSMNQVNLTCRAERFYPEDLQLIWLE
MQTFPGNNATHNWNVFIGVGVACAL 384
                           ASALPAALAVISFLLGLGLGVACVL
                                                          LGLAHS
                                                                                         KSLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALPAPPTGSALPDPQTASALPDPPA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQPEKSVSVAAGDSTVLNCTLT-----
                                                                                                                                                                                                                  PAPIEKTISKAKGQPREPQVYTLPPS----RDELTKNQVSLTCLVKGFYPSDIAVEWES
                                                                                                                                                                                                                                                SPRNITLKWFKDGQELHHLETTVNPSGKNVSYNISSTVRVV----LNSMDVHSKVICEVA
                                                                                                                                                                                                                                                                               EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                                                                                                                                                                                                             PAPEPKSCDKTHTCPELLGGPSVFLF----PPK---PKDTLMISRTPEVTCVVVDVSH--
                                                                                                                                                                                                                                                                                                                                                                          ----PRVTNVSDATKRNNMDFSIRISNVTPEDAGTYYCVKFQ-----
                                                                                                                                                                                                                                                                                                                                                                                                         LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPC
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                                                                                                                        NGNVSRN--DTPKNLTKNTDGTYNYTSLFLVNSSAHREDVVFTCQVKHDQQPAITRNHTV
                                                                                                                                                    NGQPENNYKTTPPVL--DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                               KGPSEPDTEIQSGGGTEVYVLAKPSPPEVSGPADRGIPDQKVNFTC----KSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.4%;
19.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 199; DB 1;
; Pred. No. 1.4e-05;
63; Mismatches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ----VGQSRLLIYSFTGE---HF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding; IPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SLLPVGPIK-----
                                                            ---SDQGS
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RESULT 60

SHS1_RAT

ID SHS1 RAT

AC P97710; O08951; O70426; O9QWI5;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

REPURSI OR SHPS-10 (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-1)

CO SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-1)

GN 10-OCT-2003 (Rel. 42, Last sequence update)

Experimental or SHPS-1) (Signal-1) (Sign
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as docking protein and induces translocation of PTPN6,

PTPN11 and other binding partners from the cytosol to the

plasma membrane. Supports adhesion of cerebellar neurons, neurite

outgrowth and glial cell attachment. May play a key role in

intracellular signaling during synaptogenesis and in synaptic

function. Involved in the negative regulation of receptor tyrosine

kinase-coupled cellular responses induced by cell adhesion, growth

factors or insulin. Mediates negative regulation of phagocytosis,

mast cell activation and dendritic cells and inhibits

cyrokine production by macure dendritic cells and inhibits

cyrokine production by macure dendritic cells and inhibits

the release of nitric oxide by macrophages (By similarity).

subunit: Binds pTPN1 when tyrosine-phosphorylated, except in

macrophages, where it primarily binds pTPN6. Binds GRB2 in vitro.

Binds FGR. Binds JAK2 irrespective of its phosphorylation status

and forms a stable complex. Binds SCAP1 and/or SCAP2. The

resulting complex recruits FYB. Binds PTK2B (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUBErecal LILLY PubMed=8943344;

MEDLINE=97098667; PubMed=8943344;

Fujioka Y., Matozaki T., Noguchi T., Iwamatsu A., Yamao T.,

Takahashi N., Tsuda M., Takada T., Kasuga M.;

"A novel membrane glycoprotein, SHPS-1, that binds the SH2-domain-
"A novel membrane glycoprotein phosphatase SHP-2 in response to mitog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takada T., Matozaki T., Takeda H., Fukunaga K., Noguchi T., Fujioka Y., Okazaki I., Tsuda M., Yamao T., Ochi F., Kasuga M.; "Roles of the complex formation of SHPS-1 with SHP-2 in insulin-stimulated mitogen-activated protein kinase activation.", J. Biol. Chem. 273:9234-9242(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98008865; PubMed=9344856; Ochi F., Matczaki T., Noguchi T., Fujioka Y., Yamao T., Takada T., Takuda M., Takeda H., Fukunaga K., Okabayashi Y., Kasuga M.; Tspidermal growth factor stimulates the tyrosine phosphorylation of SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing protein tyrosine phosphatase ", Biochem. Biophys. Res. Commun. 239:483-487(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-419 FROM N.A., AND TISSUE SPECIFICITY. STRAIN=WAG/Rij; TISSUE-Alveolar macrophage; MEDLINE=98375871; PubMed=9712053; Adams S., van der Laan L.J.W., Vernon-Wilson E., Renardel de Lavalette C., Doepp E.A., Dijketra C.D., van den Berg T.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>₹</u>8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYR-460; TYR-477 AND TYR-501.
MEDLINE=98204923; PubMed=9535915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Signal-regulatory protein is selectively expressed neuronal cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.,
419-429; 446-467 AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-97415431; PubMed-9271230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., SEQUENCE OF 32-48 PHOSPHORYLATION ON TYROSINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        containing protein tyrosine phosphatase and cell adhesion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION OF TYR-477 AND TYR-501,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION IN RESPONSE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Fischer 344; TISSUE=Macrophage;
MEDLINE=98449911; PubMed=9774638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sano S.-I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERACTIONS WITH PTPN6 AND PTPN11. TISSUE-Fetal fibroblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell. Biol.
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an immune antigen receptor-like molecule
Lett. 411:327-334(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          putative receptor mediating ll. Biol. 18:6213-6223(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C., Sterling H., Beckers C., Kobayashi R., Solimena M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGF, AND INTERACTION WITH PTPN11.
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AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      macrophages.";
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e brain.";
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Type I membrane protein, spleen, lung, liv
TISSUE SPECIFICITY: Highly expressed in brain, spleen, lung, liv
and kidney. Detected at lower levels in heart. Highly expressed
alveolar and peritoneal macrophages, and at lower levels in
                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 2 immunoglobulin-like C1-type domain SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: N-glycosylated.
PTM: Phosphorylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dendritic cells
                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                            the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                       adhesion or
                                                                                                                                                                                                                                                                                                                                                                                                                  ted on tyrosine residues in response to insulin, epidermal growth factors. Dephosphorylated by
                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin-like C1-type domains.
                                                                                                                                                                                                                                                                                                                         of Bioinformatics
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EMBL; D85183; BAA12734.1; -.
EMBL; D38468; BAA20368.1; -.
EMBL; D62328; AAC68478.1; -.
EMBL; AF055065; AAC18089.1; EMBL; P01703; TFAB. Repeat; Signal; Glycoprotein; Pl Pfam; PF00047; 19; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3
PROSITE; PS00290; IG_MHC; 1. InterPro; InterPro; IPR007110; Ig-like. IPR003597; Ig_cl. IPR003006; Ig_MHC. Phosphorylation Transmembrane; AAC18089.1; -Immunoglobulin domain; SH3-binding;

H T	1	FT	ΤŢ	FΤ	ŢŢ	ΕŢ	FΤ	ΨŢ	FΤ	FΤ	FΤ	FΤ	FΤ	FΤ	FΤ	FΤ	ΨŢ	FΤ	፭	FΤ	ŦΤ	ŦŢ	FΤ	FT	ΕŢ	FT	Ţ	Ϋ́	Ŧ	Ŧ	FΤ	FT	ΤŦ	FΤ	ij	Ŧ	
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	436	345	320	312	293	271	246	242	209	205	181	169	93	54	501	477		460		436	504	480	463	451	439	332	229	122	349	248	138	509	394	373		509	
F-460, F-477 AND F-501.	PHOSPHORYL	N-LINKED (GLCNAC) (POTENTIAL).	(GLCNAC) (N-LINKED (GLCNAC) (POTENTIAL).	(GLCNAC) ((GLCNAC) ((GLCNAC) (N-LINKED (GLCNAC) (POTENTIAL).	YB)	PHOSPHORYLATION (BY TYR-KINASES).	(POTENTIAL).	PHOSPHORYLATION (BY TYR-KINASES)	(POTENTIAL).	PHOSPHORYLATION (BY TYR-KINASES)	SH2-BINDING (POTENTIAL).	SH2-BINDING (POTENTIAL).	SH2-BINDING (POTENTIAL).	SH3-BINDING (POTENTIAL).	SH2-BINDING (POTENTIAL).	POTENTIAL.	POTENTIAL.		C1-TYPE	IG-LIKE C1-TYPE 1.	ĸ	CYTOPLASMIC (POTENTIAL).	POTENTIAL.	EXTRACELLULAR (POTENTIAL).	TYPE SUBSTRATE 1.	PROTEIN-TYROSINE PHOSPHATASE NON-RECEPTOR							

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RESULT 61
SRB2_HUMAI
ID SRB2
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Best Local S
Matches 105
      2_HUMAN
SRB2_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTLYVLAKP-SSPEVSGPDSRG---SPGQTVN-----FTC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS
                                                                                                                                                                                                                                                                                        DKPEHFTDNRDGTYNYTSLFLVNSSAHREDVVFTCQVEHDSQPAITENHTVRAFAHS---
                                                                                                                                                                                                                                                                                                                                YKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYTQKSLSLSPGL
                                                                                                                                                                                                                                                                                                                                                                             LNGTANFSNIIRVSP---TLKITQQPLTPASQVNLTCQVQKFYPKALQLNWLENGNLSRT
                                                                                                                                                                                                                                                                                                                                                                                                                     IEKTISKAKGQPREPQVYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGQPENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLKWLKDGKELSHLETTISSKS-NVSYNISSTVSVKLSPEDIHSRVI-CEVAHVTLEGRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -ATKRNNM----DFSICISNVTPEDAGTYYC-VKFQKGIVE-----PDTEIKSGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQADKSVSVAAGDSATLNCTVSSLTPVGPIKWFKGEGQNRSPIYSFIGGEHFPRITNVSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQGNKVVLGKKGDTVELTCTASQKKSI----QFHWKNSNQIKILGNQGSFLTKGPSKLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.1%;
                                                                                                                                                          508
                                                                                                                  384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KR -> MP (IN REF. 3; AA SEQUENCE).
G -> A (IN REF. 2).
D -> N (IN REF. 3).
N -> L (IN REF. 3; AA SEQUENCE).
N -> G (IN REF. 3; AA SEQUENCE).
G -> F (IN REF. 3; AA SEQUENCE).
E -> P (IN REF. 3; AA SEQUENCE).
NARE -> EGON (IN REF. 3; AA SEQUENCE).
R -> E (IN REF. 3; AA SEQUENCE).
NARE -> E (IN REF. 3; AA SEQUENCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYROSINE PHOSPHORYLATION AND PTPN11
BINDING. ABOLISHES TYROSINE
PHOSPHORYLATION AND PTPN11 BINDING; WI
ASSOCIATED WITH F-436, F-460 AND F-47
P-> L (IN REF. 4).
MISSING (IN REF. 3).
F-> I (IN REF. 3).
S-> C (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 192; DB 1;
Pred. No. 3.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------YGFSPR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND PTPN11 BINDING; WHEN ASSOCIATED WI'F-436, F-477 AND F-501.
Y->F: STRONGLY REDUCES INSULIN-INDUCED TYROSINE PHOSPHORYLATION AND PTPN11 BINDING. ABOLISHES TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION AND PTPN11 BINDING; WHEN ASSOCIATED WITH F-436, F-460 AND F-501. Y->F: STRONGLY REDUCES INSULIN-INDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y->F: ABOLISHES TYROSINE
           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58E1FE0A4DD429F4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 159;
        387
        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTPN11 BINDING; WHEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F-460 AND F-477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NI
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        RA Deloukas P., Matthews L.H., Abhurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.V.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley J.E., McConnachie L.J., McLay K., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Prathallingam S.R., Plumb R.W., Ramay H.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Robers J.,
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Rahas S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holtey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodrigues S. C., Grimwood J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RT Human and mouse cDNA sequences ";
RT human and mouse cDNA sequences ";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21036165; PubMed=11185750; Ichigotani Y., Matsuda S., Machida K., Oshir Yamaki K., Hayakwa T., Hamaguchi M.; Wolecular cloning of a novel human gene (SI member of the SIRP/SHPS-1 protein family."; J. Hum. Genet. 45:378-382 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9P1W8; Q8WWA5; Q9NQK8;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Signal-regulatory protein beta-2 precursor (S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21638749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NA sequence and comparative 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analysis of human chromosome 20.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oshima K., Iwamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SIRP-B2) which encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SIRP-beta-2) (SIRP-b2)
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Query Match
Best Local Sim
Matches 113;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 3.
SMART; SM00407; IGcl; 2.
SMART; SM00407; IGcl; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS50835; IG_LIKE; 3.
                                                                                                                    CONFLICT
                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                             DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB042624; BAA95692.1; -.
EMBL; AL138804; CAC00474.1; -.
EMBL; BC020629; ALT_INIT.
Genew; HGNC:15757; SIRPB2.
                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ဂ</u>
                                                                                                                                                                        VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat; Signal;
Alternative spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO:0007267; P:cell-cell signaling; TAS.
GO:0007242; P:intracellular signaling cascade; TAS.
GO:0008285; P:negative regulation of cell proliferation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 2 immunoglobulin-like C1-type domain. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note=No experimental confirmation available;
TISSUE SPECIFICITY: Detected in liver, and at very
brain, heart, lung, pancreas, kidney, placenta and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: Probable immunoglobulin-like cell surface receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  605466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9P1W8-2; Sequence=VSP_007027; Note=No experimental confirmation av
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=Q9P1W8-3; Sequence=VSP_007028;
6 PFRHLLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :soId=Q9P1W8-1; Sequence=Displayed;
                                                     Similarity
                                                                                                                                                                                                  Conservative
                                                                                                                                                                       144
                                                                                                      Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                    263
286
                                                                                                                                                                        360
                                                7.0%;
                                                                                                      42495
                                                                                                        X.
                                56;
                                                                                                                                                                     /FTId=VSP
                                                  Score 188.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                         Missing
                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                           N-LINKED
                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                              IG-LIKE V-TYPE.
IG-LIKE C1-TYPE 1.
IG-LIKE C1-TYPE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL-REGULATORY PROTEIN BETA-2
                                                                                                                  /FTId=VSP_007027.
Missing (In isoform (
/FTId=VSP_007028.
A -> V (IN REF. 2).
L -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                        /FTId=VSP
                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I membrane protein.
                                                                                                    F7F20C9F86E0E64B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin domain;
                                  Mismatches
                                                                                                                                                                                                         (in isoform
                                                                                                                                                                                                                     ) (GLCNAC...)
) (GLCNAC...)
) (GLCNAC...)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    available;
                                                  ; DB 1;
1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at very low levels
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                                Indels 173;
                                                                Length
                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skeletal
                                                                  387;
                                Gaps
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RESULT 62
SHS1BODT
ID SHS1
ID SHS1
ID SHS1
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DT 10-00
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                                                                                                                                                                                                                                                                            Brooke G.P., Parsons K.R., Howard C.J.,
"Cloning of two members of the SIRP alpha family of protein tyrosine phosphatase binding proteins in cattle that are expressed on monocyte and a subpopulation of dendritic cells and which mediate binding to CD4 T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHAIL BOVIN STANDARD; PRT; 506 AA.

046631; 046632;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Protein-tyrosine phosphatase non-receptor type substrate 1 precursor (SHP substrate-1) (Inhibitory receptor SHPS-1) (Signal-regulatory protein alpha-1) (Sirp-alpha-1) (MyD-1 antigen).

PTPNSI OR SHPSI OR SIRP OR MYD1.
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ASP-203; ARG-261;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Friesian; TISSUE=Peripheral blood
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                          as docking protein and induces translocation of PTPN6, PTPN11 and other binding partners from the cytosol to the plasma membrane. Supports adhesion of cerebellar neurons, in outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synapt. function. Involved in the negative regulation of
                                                                                                                                                                                                                        FUNCTION: Immunoglobulin-like
                                                                                                                                                                                                                                                     J. Immunol. 28:1-11(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell activation. CP47 binding prevents maturation of immature dendritic cells and inhibits cytokine production by mature dendritic cells (By similarity).

SUBUNIT: Binds PTPNI1 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPNS. Binds GRB2 in vitro. Binds JAKZ irrespective of its phosphorylation status and forms a stable complex. Binds SCAP1 and/or SCAP2. The resulting complex recruits FYB. Binds FGR and FTK2B (By similarity).

SUBCELLULAR IOCATION: Type I membrane protein.

TISSUE SPECIFICITY: Highly expressed in spleen macrophages. Detected in skin dendritic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Phosphorylated on tyrosine residues (By similarity). SIMILARITY: Contains 2 immunoglobulin-like C1-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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                                                                                                                                                                                                                                                                                                                         3M00407; IGC1; ...
; PS50835; IG_LIKE; 3.
;; PS508290; IG_MIC; FALSE_NEG.
;; Signal; Transmembrane; Immunoglobulin; Signal; Transmembrane; Polymorphism.
rotein; Phosphorylation; Polymorphism.
POTENTIAL.
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an email to license@isb-sib.ch).
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21-JUL-1986
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Selsing E., Mi "Evolution of

SEQUENCE FROM N.A.

MEDLINE-83014953; PubMed-6812053; Selsing E., Miller J., Wilson R., Storb U.; "Evolution of mousee immunoglobulin lambda g Proc. Natl. Acad. Sci. U.S.A. 79:4681-4685(

bulin lambda genes."; 79:4681-4685(1982).

MEDLINE=81148806; PubMed=6259534;

EQUENCE FROM N.A. (MOPC 315)

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Mus.

Mus musculus (Mouse)

21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-MAR-2004 (Rel. 43, Last annotation
15 lambda-1 chain C region.

on update)

STANDARD;

PRT;

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Query Match
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Matches 71
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                                                                                                                                                                                . Similarity 71; Conserv
                                                                                                                      LTVSAKPSPPVLSGPTV
DODTGOTPGPNDSNWTS
              EAQDGEL----DGLWTT
                            VFVENKDGTFNQTSWFLVNSSAHREAVVLTCQVEHDG-----QPAVSKNHTLEVSAPQK
                                           PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCA
                                                                                                      VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA--PIEKTISKA
                                                                                                                                   SCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH--EDPEVKFNWYVDG
                                                                                                                                                  PRVTNVSDATKRNNMDFSIRISNITPADAGVYYCVKFRKEERGDMEFK-----SGPGTH
                                                                                                                                                          PRGKNIQGGK-----TLSVSQLELQDSGTWTCTVLQNQKK--VEFKIDIVPCPAPEPK
                                                                        KGQPREPQVYTLPPSRDELT-----KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                        NELSASQTSVDPEDNNVSYSINSTTKVLLATGDVHSQVICEVAHVTLQGGPPL-----
                                                          RGTANLSETIRVPPTL-EITGSPSAGNQVNVTCQVNKFYPRHLQLTWLENGNMSRTEAAS
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371
              452
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Pred. No. 6.3e
52; Mismatches
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N -> S.
T -> A.
S -> L.
K -> R.
Y -> H.
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                                                                                                                                                                                6.3e-05;
ches 139;
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RESULT 64
VCA1_RAT
ID VCA1_RAT
AC P29534;
DT 01-APR-1993
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"Amino acid sequences of two mouse immunoglobulin lambda chains.";

Proc. Natl. Acad. Sci. U.S.A. 68:590-594(1971).

-I- MISCELLANEOUS: The MOPC 315 cell line produces 2 light chains, 1 normal lambda-2 chain and 1 abnormal lambda-1 chain that is missing a large part of the V region. The C region sequence (shown here) appears completely normal.

-I- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00582; AAA51636.1; -.
EMBL; J00587; AAB59672.1; -.
PIR; A93922; L1MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entitles requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (S43).
MEDLINE=82220143; PubMed=6283385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bothwell A.L.M., Paskind
Gefter M.L., Baltimore D
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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MEDLINE=71107854; PubMed=5276767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Somatic variants of murine immunoglobulin lambda light chains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Dual expression of lambda Nature 290:65-67(1981).
                                                                                                                   385
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                                                                                                                                            \vdash
                                                                                                                                                                                            l Similarity
37; Conserv
                                                                                                                                                     QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD
                                                                                                                SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                         QPKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQ
                                                                                         SNNKYMASSYLTLTARAWERHSSYSCOVTHE---GHTVEKSLS
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104
19
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96
  (Rel. 25, Created)
                                                                                                                                                                                              Conservative
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                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                         domain; Immunoglobulin C region; 3D-structure.
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                                                                                                                                                                                                                                             ET -> TE (IN REF. 4).

Q -> E (IN REF. 4).

MISSING (IN REF. 4).

HS -> SH (IN REF. 4).

S -> SS (IN REF. 4).

E -> Q (IN REF. 4).

E -> Q (IN REF. 4).
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                                                                                                                                                                                                        Score 177.5;
Pred. No. 4.4
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                                                                                                                                                                                                                                                                                                                                     INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                IG-LIKE.
                          PRT;
                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M., Imanishi-Kari T., Rajewsky K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the MOPC-315 plasmacytoma.";
                          739
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                                                                                                                                                                                                                    DB 1;
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PRINTS; PR01474; VCAM1.
SMART; SM00408; IGC2; 3.
PR0SITE; PS50835; IG LIKE;
Immunoglobulin domain; Glyc
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M84488; AAA423:
PIR; JS0675; JS0675.
HSSP; P19320; 1VCA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE 97.007., "Tizard R., Chisholm P., Williams C., Mysa P., Burkly L., Mysak K., Kincade P., Lobb R.;
Burkly L., Miyake K., Kincade P., Lobb R.;
"Cloning of murine and rat vascular cell adhesion molecule-1.";
"Cloning of murine Res. Commun. 183:163-169(1992).

Biochem. Biophys. Res. Commun. 183:163-169(1992).

1- FUNCTION: IMPORTANT IN CELL-CELL RECOGNITION. APPEARS TO FUNCTION.

1- FUNCTION: METH. THE BETA.
                                                                                                                                                                                                                                                                   Repeat; Signal.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and inflamed tissue.
-!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
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Mammalia; Eutheria;
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VCAM1 OR VCAM-1.
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10-OCT-2003
                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                         TRANSMEM
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InterPro; IPR0037110; Ig-like.
InterPro; IPR003988; Ig c2.
InterPro; IPR003989; VCAM-1.
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                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGITRANSDICTION. THE VCAMI/VLA4 INTERACTION MAY PLAY A PATHOPHYSIOLOGIC ROLE BOTH IN IMMUNE RESPONSES AND IN LEUKOCYTE ENIGRATION TO SITES OF INFLAMMATION. SUBCELLULAR LOCATION: Type I membrane protein. TISSUE SPECIFICITY: Expressed on inflamed vascular endothelium, well as on macrophage-like and dendritic cell types in both norm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
ll adhesion protein 1 precursor (V-CAM
                119
223
312
312
408
6014
6014
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273
273
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                          Chordata;
Rodentia;
81246 MW;
                                                                                                                                                                                                                                                                                            Glycoprotein; Cell adhesion; Transmembrane;
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         IG-LIKE C2-TYPE 1
IG-LIKE C2-TYPE 2
IG-LIKE C2-TYPE 3
IG-LIKE C2-TYPE 4
IG-LIKE C2-TYPE 5
IG-LIKE C2-TYPE 6
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VASCULAR CELL
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Sciurognathi; Muridae; Murinae; Rattus.
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(GLCNAC.
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE PAREAUX, MEDILINE PROTECTION (NEW YORK NEW YORK 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Basement membrane-specific heparan sulfate proteoglycan protein precursor (HSPG) (Perlecan) (PLC).
                 Nicole
                                                                                        basement membrane (HSPG2/perlecan). A chimeric molecule with multiple domains homologous to the low density lipoprotein receptor, laminin, neural cell adhesion molecules, and epidermal growth factor.";

J. Biol. Chem. 267:8544-8557(1992).
                                                                                                                                                                                                     MEDLINE=92235084; PubMed=1569102;
Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., I
"Primary structure of the human heparan sulfate
                                                                                                                                                                                                                                                                                                                                                          467-kD protein containing multiple domains low density lipoprotein receptor, laminin, molecules, and epidermal growth factor."; J. Cell Biol. 116:559-571(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=92112994; PubMed=1730768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia; |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P98160; Q16287; Q9H3V5;
01-OCT-1996 (Rel. 34, C
                                   MEDLINE=20553141;
                                                            SEQUENCE OF 22-4391 FROM N.A.,
                                                                                                                                                                                                                                                                                     TISSUE=Colon,
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malia; Eutheria; F
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PubMed=11101850;
e C.-S., Topalogin "
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Primates;
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            L., Barral
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Dodge G.F
                                                                                                                                    AND O-LINKED OLIGOSACCHARIDES.

-!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel syndrome (SJS1) [MIM:255800]; a rarre autosomal recessive disordaracterized by permanent myotonia (prolonged failure of must relaxation) and skeletal dysplasia, resulting in reduced state kyphoscoliosis, bowing of the diaphyses and irregular epiphyse -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
-!- SIMILARITY: Contains 3 laminin EGP-like domains.
-!- SIMILARITY: Contains 3 laminin IV domains.
-!- SIMILARITY: Contains 3 laminin G-like domains.
-!- SIMILARITY: Contains 4 EGP-like domains.
-!- SIMILARITY: Contains 1 SEA domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beighton P., Ben-Hamida C., Hammou Samson D., Urtizberea J.A., Lehmar Hentati F., Fontaine B.; "Perlecan, the major proteoglycan patients with Schwartz-Jampel sync
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang H., Li X.-J., Martin D.B., Aebersold R.; "Identification and quantification of N-linked glycoproteins "Identification chemistry, stable isotope labeling and mass spectro Nat. Biotechnol. 21:660-666 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of human heparan sulfate proteoglycan core assignment of the gene (HSPG2) to 1p36.1-->p35 and a BamHI restriction fragment length polymorphism."; Genomics 11:389-396(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Heparan sulfate proteoglycan of human colon: partial cloning, cellular expression, and mapping of the gene short arm of human chromosome 1."; Genomics 10:673-680(1991).
                                                                                             between
                                                                                                        This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYDRATE-LINKAGE SITE ASN-2121.
MEDLINE-22660472; PubMed=12754519;
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"Structural characterization
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MEDLINE=94052171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [SSUE=Fibrosarcoma;
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                                                                       s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EW European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: Found in the basement membranes.
PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration
                                                                                                                                                                                                                                                                                                                                                                                                         properties. It serves as an attachment substrate for cells. SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement membrane components such as laminin, prolargin and collagen type
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F., Iozzo R.V.;
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Lehmann-Horn
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DR EMBL, MA2519, CAA44793.1; ...

DR EMBL, MA45799; CAC18934.1; ...

DR SERL, MA45799; CAC18934.1; ...

DR SERL, MA45799; CAC18934.1; ...

DR SERL, MA4579; AMBOTATED_COS.

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RESIDE CONTROL OF CONT	DD QY	B & 8	5	Q Db Q	B 8	β Q	Db 42	A AG	
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                                                                                         SEQUENCE OF 158-383 (MYELOMA PROTEIN MEDLINE=81223768; PubMed=6787589; Lin L.-C., Putnam F.W.;
                                                                                                                                                                                                                Putnam F.W., Takahashi N., Tetaert D., Deburge B., "Amino acid sequence of the first constant region of the dalta heavy chain of human IgD hinge region of the dalta heavy chain of human IgD proc. Natl. Acad. Sci. U.S.A. 78:6168-6172(1981).
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MEDLINE=82082419; PubMed=6947220;
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Biochem. Biophys. Res. Commun. 97:635-641(1980)
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Shinoda T., Takahashi N., Takayasu T.
"Complete amino acid sequence of the
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                           ATTRNTGRGGEEKKKEKEEGEERETKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFT
                                                            STPLQQWRQG-EYKCVVQHTASKSKKEIFRWPESPKAQASSVPTAQPQAEGSLAKATTAP
                                                                                             PKD-----NSPVVLACLI-TGYHPTSVTVTWYM-GTQSQPQRTFPEIQRRDSYYMTSSQL
                                                                                                              PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
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IG-LIKE 3.
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                                                                                                                                                                  DA1DE73519C76C1D
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of a human
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                                         YTLPPSRDEL-TKNQVSLT
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   RESULT 68
CD22_HUMAN
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Stamenkovic I., So
"The B-cell antigo
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P20273; O95699; O95701; O95702; O95703; Q01665; Q92872; Q92873;
Q9UQA7; Q9UQA8; Q9UQA9; Q9UQA9; Q9Y2A6;
01-FEB-1991 (Rel. 17, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
B-cell receptor CD22 precursor (Leu-14) (B-lymphocyte cell adhesion molecule) (BL-CAM) (Siglec-2).
                                      MEDLINE=93216636; PubMed=8463235; Powell L.D. Sgroi D. Sjoberg E.R., Stamenkovic I., Varki A.; Prowell L.D. Sgroi D. Sjoberg E.R., Stamenkovic I., Varki A.; "Natural ligands of the B cell adhesion molecule CD22 beta carry N-linked oligosaccharides with alpha-2,6-linked sialic acids that required for recognition."; J. Biol. Chem. 268:7019-7027(1993).
                                                                                                                                                                                                                                      SEQUENCE OF 13-137; 139-239; 241-328 AND 418-502 FRO VARIANTS THR-34; GLU-152; LYS-203; GLY-664; CYS-669
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS CD22-ALPHA AND CD22-BETA).
Lamerdin J.E., McCready P., Adamson A.W., Burkhart-Schultz
Garcia E., Kyle A., Ramirez M., Stilwagen S., Garnes J.,
Danganan L., Bruce R., Quan G., Montgomery M., Ow D.,
INTERACTION WITH I MEDLINE=95343349;
                                                                                                                                                                                         MEDLINE-99180618; PubMed=10079291
Hatta Y., Tsuchiya N., Matsushita
Tokunaga K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS CD2: MEDLINE=93267103; PubMed=8496602
                                                                                                                                   SIALIC ACID BINDING
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                                                                                                                                                                mmunogenetics
                                                                                                                                                                             Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vilson G.L., Fox C.H., Fauci A.S., Ke CDNA cloning of the B cell membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure and chromosomal ol. 150:5013-5024(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FSPPNILLMWLEDQREVNTSGFAPARPPPQPGSTTFWAWSVLRVPAPP--SPQPATYTCV
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                                                                                                                                                                                                                                                                                                                                                                       A., Olsen A.O., Carrano A.V.; (AUG-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                                                                                                                            of the gene variations
49:280-286(1999).
                                                                                                                                                                                                                                                                                                              Seed
             PTPN6
 PubMed=7618087;
                                                                                                                                                                                                                                                                                                                              PubMed=1691828;
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                                                                                                                                                                                                                                                                                                                                            (ISOFORM CD22-BETA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mapping of the
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Annu Sev. Immunol. 51:481-504 (1997).

Annu Rev. Immunol. 15:481-504 (1997).

C -!- FUNCTION: Mediates B-cell bin lymphoid tissues. Binds sialylated the localization of B-cells in Lymphoid tissues. Binds sialylated glycoproteins; one of which is CD45. Preferentially binds to alpha2,6-linked sialic acid. The sialic acid recognition site can be masked by cis interactions with sialic acids on the same cell surface. Upon ligand induced trosine phosphorylation in the immune response seems to be involved in regulation of B cell antigen receptor signaling. Plays a role in positive regulation through interaction with Src family tyrosine kinases and may also act as an inhibitory receptor by recruiting cytoplasmic phosphatases via their SH2 domains that block signal transduction through dephosphorylation of signaling molecules.

-!- SUBUNIT: Predominantly monomer of isoform CD22-beta. Also found as heterodimer of isoform CD22-beta and a shorter isoform. Interacts with PTPN6/SHP-1, LYN, SYK, PIKNRI/PIKNR2 and PLCG1 upon phosphorylation. Interacts with GRB2, INPSD and SHC1.

C phosphorylation (By similarity). May form a complex with INPSD/JSHIP, GRB2 and SHC1.

C INPSD/JSHIP, GRB2 and SHC1.

C FUNCTION: Type I membrane protein.

C FUNCTION: Type I membrane protein.
   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen receptor signaling.";
Annu. Rev. Immunol. 15:481-504(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTION WITH PTPN6; SYK AND PLCG1.
MEDLINE=96195207; PubMed=8627166;
Law C.L., Sidorenko S.P., Chandran K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96257803; PubMed=8647200;
Tuscano J.M., Engel P., Tedder T.F., Agarwal
"Involvement of p72syk kinase, p53/56lyn kina
inositol-3 kinase in signal transduction via
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphatase SHP.";
Science 269:242-244(1995)
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Fischer B.H., Clark E.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "CD22 associates with protein tyrosine phosphatase phospholipase C-gamma(1) upon B cell activation."; J. Exp. Med. 183:547-560(1996).
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                                                   PTM: Phosphorylated on tyrosine residues by LYN (i
SIMILARITY: Belongs to the immunoglobulin superfan
(sialic acid binding Ig-like lectin) family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type
SIMILARITY: Contains 1 immunoglobulin-like V-type
CAUTION: Ref.4 sequence differs from that shown di
frameshift in position 806.
DATABBASE: NAME-PROW: NOTE-CD guide CD22 entry;
                                                                                                                                                                                                                   Name=CD22-alpha;
IsoId=P20273-2; Sequence=VSP 002531;
TISSUE SPECIFICITY: B lymphocytes.
DOWAIN: Contains 4 copies of a cytoplasmic motif that is referred to as the immunoreceptor tyrosine-based inhibitor motif (ITIM). This motif is involved in downmodulation of cellular responses. The phosphorylated ITIM motif binds to the SH2 domain of PTPM6/SHP-1.
PTM: Phosphorylated both on threonine/serine and tyrosine
                                  DATABASE: NAME=PROW; NOTE=CD guide CD22 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd22.htm"
                                                                                                                                                                                                                                                                                                                                                                                                        Name=CD22-beta;
                                                                                                                                                                                                    residues.
   SWISS-PROT
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ano J., Sato S.,
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copyright.
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via the human B lymphocyte
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EMBL; X59350; CAA42006.1; -.

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R EMBL; U62631; AAB06449.1; -.

R EMBL; M62631; AAB0645.1; -.

DR EMBL; AB01299; BAA36565.1; -.

DR EMBL; AB012999; BAA36566.1; -.

DR EMBL; AB012999; BAA36568.1; -.

DR EMBL; AB012999; BAA36568.1; -.

DR EMBL; AB013009; BAA365671.1; -.

DR EMBL; AB013000; BAA36573.1; -.

DR EMBL; AB013003; BAA36573.1; -.

DR EMBL; AB013004; BAA36573.1; -.

DR EMBL; AB013004; BAA36573.1; -.
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InterPro; IPR003598; Ig_c2.
Pfam; PF00047; ig; 6.
SMART; SM00408; IGc2; 4.
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32 KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGN
                  95;
                           Similarity
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                          6.2%;
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Repeat; I
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                 70;
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BY SIMILARITY:
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                Score 167; DB 1;
Pred. No. 0.0028;
0; Mismatches 15
                                                   (INVOLVED IN BINDING TO SYK, P PIK3R1/PIK3R2) (BY SIMILARITY) N-LINKED (GLCNAC. . .) (POTENT
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CYTOPLASMIC (POTENTIAL).
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Phosphorylation;
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                                  DB 1;
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                 154;
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                                  Length 847;
                 Indels 130;
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                                                    (POTENTIAL).
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                                                                                                                                                      SYK)
                                                                     PLCG2
                 Gaps
91
                 23;
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RESULT

HUMAN

SRB1 HUMAN STANDARD; PRT; 398 AA.

000241; QBTB12; Q9H1U5; Q9Y4V0;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Signal-regulatory protein beta-1 precursor (S

Homo sapiens (Human) Eukaryota; Metazoa;

Mammalia; Eutheria;

Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

(SIRP-beta-1)

Chordata;

NCBI_TaxID=9606;

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                                                                                  AVEWESNG----- OPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL
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                                                                                                                              KCKVSNK--ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
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Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Ash Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Ash Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clark S.Y., Clee C.M., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Chapman J.C., Collier M.E., Connor R.E., Corby N.R., Collson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ash Coulson A.G., Frankland J.A., Fraser A., French L., Garner P., Ash Ellingron A.G., Frankland J.A., Fraser A., French L., Garner P., Ash Ellingron A.G., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Kay M.P., King A., Knights A., Laird G.K., Lawlor S., Kay M.P., King A., Knights A., Laird G.K., Lawlor S., King A., King A., Knights A., Laird G.K., Lawlor S., King A., King 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=21638749; PubMed=11780052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A family of proteins that receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta; MEDLINE=97215901;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Chen Z., Sures I.,
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Willalon D.K., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Shevjanski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
  modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH TYROBP, N-GLYCOSYLATION, AND TISSUE SPECIFICITY.
MEDLINE=20072721; PubMed=10604995;
Dietrich J., Cella M., Seiffert M., Buehring H.-J., Colonna M.;
"Signal-regulatory protein beta 1 is a DAP12-associated activating receptor expressed in myeloid cells.";
J. Immunol. 164:9-12(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.B., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Whittaker P., Willey D.L., Beck S., Beck S., Walling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tomasello E., Cant C., Buehring H.-J., Vely F., Andre P., Seiffert M Ullrich A., Vivier E., "Resociation of signal-regulatory proteins beta with KARAP/DAP-12."; Eur. J. Immunol. 30:2147-2156(2000).
                                                                   between
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                                                                                                                  PTM: N-glycosylated.
SIMILARITY: Contains 2 immunoglobulin-like C1-type domain.
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Immunoglobulin-like cell surface receptor involved the negative regulation of receptor tyrosine kinase-coupled signaling processes. Participates also in the recruitment of tyrosine kinase SYK.
                                    ween the Swiss Institute of Bioinf.
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Interacts with TYROBP. This interaction recruitment of SYK.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                               TISSUE
                                                                                                                                                                                                                                                                                                                           Event-Alternative
                                                        SWISS-PROT entry is copyright. It is produ
                                                                                                                                                                                        IsoId=000241-2; Sequence=VSP_007026;
Note=No experimental confirmation available;
SSUE SPECIFICITY: Detected in monocytes and
                                                                                                                                                                                                                                                                              IsoId=000241-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NA sequence and comparative analysis of human chromosome 20.", 414:865-871(2001).
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Feingold E.A., Grouse L.H.,
                      institutions as
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EMBL; AL1049634; CAR3-6661.2; -.
EMBL; AL138804; CAC17540.1; -.
EMBL; BC025286; AAR25286.1; -.
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Signal; Transmembrane; Immunoglobulin Alternative splicing.
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GO; GO:0007166; P:cell surface receptor linked signal transdu.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-cl.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                          Similarity
                     QKSLSLSPGLQLDETCAEAQDGELDGLWTTDPPRASALP
                                                                                                                                                                                               EFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                                                                         GOSLITLILESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ--NQKKV
                                          QLTWLENGNVSRTETASTLIENKDGTYNWMSWLLVNTCAHRDDVVLTCQVEHDG
                                                              AVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                                                                                    CEMAHITLQGDPLRGTANLSEAIRVPPTLEV-TQQPMRAE---NQANVTCQVSNFYPRGL
                                                                                                        CKVSNKALPA-PIEKT--ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDI
                                                                                                                                GFSPRDITLKWFKNGNELSDFQTNVDPAGDSVSYSIHSTARVVLTRGDVHSQVI-----
                                                                                                                                                    --EDPEVKFNWYVDGVEVHNAKTK--PREE----QYNSTYRVVSVLTVLHQDWLNGKEYK
                                                                                                                                                                          EFK-----SGAGTELSVRAKPSAP-VVSGPAV------RATPEHTVSFTCESH
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SAHQKEHGSDITHEPALAPTAP
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                                                                                                                                                                                                                                                               Score 166.5; |
Pred. No. 0.00
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (In isoform 2
/FIIG-VSP 007028.
R -> H (IN REF 2) CA
D -> N (IN REF 1).
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SIGNAL-REGULATORY PROTEIN
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-LIKE V-TYPE
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RESULT 70 UN89_CAEEL ID UN89_C AC 001761

UN89 CAEEL 001761; Q17362

STANDARD

PRT;

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WormPep; C09DL1; C330426.
InterPro; IPR003957; FN III-like.
InterPro; IPR003961; FN III-
InterPro; IPR003961; FN III.
InterPro; IPR003710; Ig-like.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR00306; Ig MHC.
InterPro; IPR001849; PH.
InterPro; IPR001849; RhoGEF.
InterPro; IPR001452; SH3.
Pfam; PF00047; Ig; 47.
Pfam; PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF0018; SH3; 1.
SMART; SM00308; IGC2; 23.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00325; RhoGEF; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50010; DH 2; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
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[2]
SEQUENCE FROM N.A.
STRAIN=Bristol N2;
Du Z., Le T.T., Wilson R
Submitted (MAY-1997) to
[3]
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U33058; AAB01
EMBL; AF003131; AAI
PDB; 1FHO; 20-DEC-(
WOrmPep; C09D1.1; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified entities
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Submitted
-!- FUNCTI
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STRAIN=96180278; PubMed=8603916;
Benian G.M., Tinley T.L., Tang X., Borodovsky M.;
"The Caenorhabditis elegans gene unc-89, required assembly, encodes a giant modular protein composed transduction domains.";
J. Cell Biol. 132:835-848(1996).
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Muscle M-line assembly protein unc-89 (Uncc UNC-89 OR COSD1.1.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   58; AAB00542.1; -.
3131; AAB54132.2;
20-DEC-00.
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JONAIN INTERPRETATION IN
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RCSD 3.

RCSD 3.

RCSD 4.

RCSD 4.

RCSD 4.

RCSD 5.

IG-LIKE C2-TYPE 9.

IG-LIKE C2-TYPE 11.

IG-LIKE C2-TYPE 12.

IG-LIKE C2-TYPE 20.

IG-LIKE C2-TYPE 21.

IG-LIKE C2-TYPE 21.

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IG-LIKE C2-TYPE 33.

IG-LIKE C2-TYPE 33.

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IG-LIKE C2-TYPE 34.

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IG-LIKE C2-TYPE 34.

IG-LIKE C2-TYPE 41.

IG-LIKE C2
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation updat Ig lambda-3 chain C region.
  SEQUENCE FROM N.A. MEDLINE=83014953; PubMed=6812053;
                                                                                                       Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
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                                                                                NCBI_TaxID=10090;
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Pred. No. 0.059
59; Mismatches
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L -> F (IN REF. 1).
F -> L (IN REF. 1).
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POTENTIAL.
                                                                                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262D3EDD62960E89
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RESULT 72
PGBM_MOUSE
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                  PGBM_MOUSE
Q05793;
Q1-NOV-1995
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DISULFID
SEQUENCE
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NON TER 1
DOMAIN 6
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Breyer R.M., Sauer R.T., Eisen H.N.;
"The variable region of mouse lambda-3 chains.";
"The variable region of mouse lambda-3 chains.";
"The variable region of mouse lambda-3 chains.";
                                                                                                                                                             protein precursor HSPG2.
                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 1g; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Evolution of mouse immunoglobulin
Proc. Natl. Acad. Sci. U.S.A. 79:46
[2]
SEQUENCE FROM N.A. TISSUE=Melanoma;
                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                 Basement
                                                                                                                                                                                                                                   01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
10-OCT-2003 (Rel.
                                                             NCBI_TaxID=10090;
                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; B93922; L3MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; J00585; AAB59670.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-18 (MYELOMA PROTEIN CBPC-49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=81223782; PubMed=6165998;
Azuma T., Steiner L.A., Eisen H.N.;
"Identification of a third type of lambda light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lmmunoglobulins.";
roc. Natl. Acad. Sci. U.S.A. 78:569-573(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPRE-PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QPKSTPTLTMFPPSPEELQENKATLVCLISNFSPSGVTVAWKANGTPITQGVDTSNPTKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNKYMASSFLHLTSDQWRSHNSFTCQVTHE---GDTVEKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR007110; Ig-like.
IPR003597; Ig_c1.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104
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6
27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                 32, Created)
32, Last sequence update)
42, Last annotation update)
-specific heparan sulfate pr
(HSPG) (Perlecan) (PLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 I
11371 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 163; DB
Pred. No. 0.00
16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH HEAVY CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE
                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bulin lambda genes.";
79:4681-4685(1982).
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.00037;
                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                            proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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EMBL; M77174; AAA39911.1; -.

EMBL; J04054; AAA3989.1; -.

EMBL; J04055; AAA39912.1; -.

PIR; S1852; S18252.

PDB; IGL4; 28-MOV-01.

MGD; MGI:96257; H8pg2.

GO; GO:0005604; C:basement membrane; IDA.

GO; GO:0008104; P:protein localization; IMP.

InterPro; IPR000985; ConA like_lec_g1.

InterPro; IPR000742; EGF 2.

InterPro; IPR000710; Ig-like.

InterPro; IPR000710; Ig-like.

InterPro; IPR00034; Laminin B.

InterPro; IPR00034; Laminin G.

InterPro; IPR000179; Laminin G.

InterPro; IPR00179; Laminin G.

InterPro; IPR00179; Laminin G.

InterPro; IPR00179; LDL_receptor_A.

InterPro; IPR00179; LDL_receptor_A.

InterPro; IPR00179; EGF; 4.
         Pfam; PF00008; EGF; 4.

Pfam; PF000047; 19; 15.

Pfam; PF00052; laminin_B; 3.

Pfam; PF00053; laminin_GGF; 7.

Pfam; PF00054; laminin_G; 3.

Pfam; PF00057; ldl_recept_a; 4.

Pfam; PF01390; SEA; 1.

Pfam; PF01390; SEA; 1.

PFANTYS; PR00261; LDLRECEPTOR.

PROMART; SM00180; EGF Lam; 7.

SMART; SM00180; IGC7; 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 266
[2]
SEQUENCE OF 940-169
MEDLINE=89034110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  basement
J. Biol.
-!- FUNCT
                                                                                                                                                                                                                                                                                                                                                                                                entities
or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete sequence of perlecan, a basement membrane heparan sulfate proteoglycan, reveals extensive similarity with laminin A chain, low density lipoprotein-receptor, and the neural cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Noonan D.M., Fulle
Yamada Y., Hassell
"The complete seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND O-LINKED OLIGOSACCHARIDES.
SIMILARITY: Contains 4 LDL-receptor class A domains.
SIMILARITY: Contains 11 laminin EGF-like domains.
SIMILARITY: Contains 3 laminin IV domains.
SIMILARITY: Contains 3 laminin in Collike C2-type of SIMILARITY: Contains 15 immunoglobulin-like C2-type of SIMILARITY: Contains 1 laminin G-like domains.
SIMILARITY: Contains 1 EGF-like domain.
SIMILARITY: Contains 1 SEA domain.
                                                                                                                                                                                                                                                                                                                                                                                                                       ween the Swiss Institute of Bioinformat
Buropean Bioinformatics Institute. The
by non-profit institutions as long
ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Extracellular. TISSUE SPECIFICITY: Found in the bas PTM: CONTAINS THREE HEPARAN SULFATE AND O-LINKED OLIGOSACCHARIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: This protein is an integral component of basement membranes. It is responsible for the fixed negative electrostatic charge and is involved in the charge-selective ultrafiltration properties. It serves as an attachment substrate for cells. SUBUNIT: Purified perlecan has a strong tendency to aggregate in dimers or stellate structures. It interacts with other basement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane components such as laminin, prolargin and collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collable of the Swiss Institute of Bioinformatics and the EMBL outset European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                              s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UE SPECIFICITY: Found in the basement membranes CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL
                                                           ldl_recept_a; 4.
SEA; 1.
: IGc2; )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266:22939-22947(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horigan E.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Usage
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SMART; SM00282; LamG; 3.

SMART; SM00209; LDLa; 4.

SMART; SM00200; SEA; 1.

SMORT; SM00200; SEA; 1.

PROSITE; PS00022; EGF 1; 8.

PROSITE; PS01186; EGF-2; 4.

PROSITE; PS50026; EGF-3; 4.

PROSITE; PS50025; LAM G DOMAIN; 3.

PROSITE; PS01248; LAMININ TYPE EGF; 11

PROSITE; PS01024; LAMININ TYPE EGF; 11

PROSITE; PS01024; SEA; 1.

PROSITE; PS01024; SEA; 1.
  DISULFID
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SM00282;
SM00192;
SM00200;
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LDL-RECEPTOR CLASS A 2.
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LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
IG-LIKE C2-TYPE 1.
LAMININ EGF-LIKE 1 (N-TERMINAL).
LAMININ EGF-LIKE 1 (C-TERMINAL).
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4 (INCOMPLETE).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 5 (N-TERMINAL).
LAMININ EGF-LIKE 6.
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LAMININ EGF-LIKE 6.
LAMININ EGF-LIKE 7
LAMININ EGF-LIKE 9 (N-TERMINAL).
LAMININ EGF-LIKE 9 (N-TERMINAL).
LAMININ EGF-LIKE 9 (N-TERMINAL).
LAMININ EGF-LIKE 10.
LIKE C2-TYPE 10.
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                                                            MP--IKVEWKIRDQELEDNVHISP-----NGSITTIVAPGPATMEPTACVASNVYGMAQS
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RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetcow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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"Genomic structure of the human Ig lambda 1 gene suggests that it be expressed as an Ig lambda 14.1-like protein or as a canonical E cell Ig lambda light chain: implications for Ig lambda gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Immunoglobulin lambda light-chain-related genes 14.1 and 16.1 expressed in pre-B cells and may encode the human immunoglobuli omega light-chain protein."; proc. Natl. Acad. Sci. U.S.A. 86:5552-5556(1989).
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MEDLINE=89315835; PubMed=2501791;
Rvans R.J., Stafford-Hollis J.M.,
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01-APR-1990 (Rel. 14, Last sequence update)
11-APR-1990 (Rel. 14, Last sequence update)
15-MAR-2094 (Rel. 43, Last annotation update)
Immunoglobulin lambda-like polypeptide 1 precursor (Immunoglobulin-related 14.1 protein) (Immunoglobulin omega polypeptide) (Lambda 5)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=83014953; PubMed=6812053;
MEDLINE=83014953; PubMed=6812053;
Selsing E., Miller J., Wilson R., Storb U.;
Selsing E., Miller J., Wilson R., Storb U.;
"Evolution of mouse immunoglobulin lambda genes.";
"Evolution of mouse immunoglobulin lambda genes.";
"Evolution of mouse immunoglobulin lambda genes.";
"Anarl. Acad. Sci. U.S.A. 79:4681-4685(1982).
                                                                                                                                                                                                                                                                                     LAC2 MOU
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MEDLINE=82220143;
                                           MEDLINE=82274221; PubMed=6287422; Wu G.E., Govindji N., Hozumi N., Muria "Nucleotide sequence of a chromosomal immunoglobulin gene of mouse ",
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                            Mus musculus (Mouse)
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21-JUL-1986 (Rel. 01,
10-OCT-2003 (Rel. 42,
Ig lambda-2 chain C re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:5870; IGLL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; BC012293; AAH12293.1;
PIR; A33911; A33911.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M34513; AAA36096.1; -...
EMBL; M34511; AAA36096.1; JOINED.
EMBL; M34512; AAA36096.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 146770; -.
GO:0016020; C:membrane; NAS.
GO:0003793; F:defense/immunity protein activity; NAS.
GO:0006955; P:immune response; NAS.
                                                                                                                                                                                         _TaxID=10090;
                                                                                                                                                                                                                                                                                                  MOUSE
                                                                                                                                                                                                                                                                                                                                                                                   385
                                                                                                                                                                                                                                                                                                                                                                                                                               327
                                                                                                                                                                                                                                                                                                                                                           169
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                                   Acids
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            FROM
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1 37 PO1
                                                                                                                                                                                                                                                                                                                                                           SNNKYAASSYLSLTPEQWRSRRSYSCQVMHE-----
                                                                                                                                                                                                                                                                                                                                                                                SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQ
                                                                                                                                                                                                                                                                                                                                                                                                       QPKATPSVTLFPPSSEELQANKATLVCLMNDFYPGILTVTWKADGTPITQGVEMTTPSKQ 168
                                                                                                                                                                                                                                                                                                                                                                                                                               QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50835; IG_LIKE; 1. PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
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           N.A.
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PubMed=6283385;
                                  10:3831-3843 (1982)
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108
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            (MOPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 162.5; I
Pred. No. 0.00;
21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMUNOGLOBULIN LAMBDA-LIKE J REGION (BY SIMILARITY TO LIGHT-CHAIN).

C REGION (BY SIMILARITY TO LIGHT-CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9133A7742B943C79
                                                                     Murialdo
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                                                                                                                                                                                                                                                                                                 104
                                                                                                                                                                                                                                                 update)
                                                          rearranged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .00097;
                                                                     Η.
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                                                          lambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
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                                                                                                                                                                                                                                                                                                                                                           211
                                                                                                                                                                                                                                                                                                                                                                                442
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Eukaryota; Metazoa; Mammalia; Eutheria;

Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;

Euteleostomi Sus.

haplotype

U

beta chain

NCBI_TaxID=9823;

SEQUENCE FROM N.A.

Sus scrofa (Pig). precursor.

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RP OCC OCC DET DIC
                                                                                                                                                       RESULT 75
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Best Local
                                                                                                                                  HB2D PIO
                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SLA class II histocompatibility antigen, DQ h
                                                                                                                                                                                                                                                                                                                                                                   DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no reat use by non-profit institutions as general as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00595; AAA39151.1; PIR; C93922; L2MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=81223782; PubMed=6165998; Azuma T., Steiner L.A., Eisen H.N
                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin
NON_TER ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of a third type of lambda light chain immunoglobulins.";
Proc. Natl. Acad. Sci. U.S.A. 78:569-573(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 66-104 (MOPC 315), AI MEDLINE=81223782; PubMed=6165998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dugan E.S.,
"Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dugan E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=74048693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bothwell A.L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                              PIG
                                                                                                                                                                                                                                    386
                                                                                                                                                                                                                                                                                  327
                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                         l Similarity
35; Conserv
                                                                                                                                                                                                                                 DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                        QPRE-PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS
                                                                                                                                                                                                         GNKFMASSFLHLTSDQWRSHNSFTCQVTHE---GDTVEKSLS
                                                                                                                                                                                                                                                        QPKSTPTLTVFPPSSEELKENKATLVCLISNFSPSGVTVAWKANGTPITQGVDTSNPTKE
                                                                                                                                                                                                                                                                                                                                                         104 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradshaw R.A., Simms E.S., Eisen H.N., sequence of the light chain of a mouse
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12:5400-5416(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                    domain;
                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=4760498;
naw R.A., Simms E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of.
                                                                                                                                                                                                                                                                                                                                                                     103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Ig-like.
; Ig_cl.
; Ig_MHC.
                                                                                                                                                                                                                                                                                                                   6.0%;
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99
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                                                                                                                                                                                                                                                                                                                      Score 161;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                    Pred.
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                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                    region.
                                                                                                                                             A
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                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                             Length 104;
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Best Local S
Matches 46
                                                             01-NOV-1990 (Rel. 16, Cat 01-NOV-1990 (Rel. 16, Lat 10-OCT-2003 (Rel. 42, Lat Vascular cell adhesion procession).
                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM DOMAIN DISULFID DISULFID CARBOHYD SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom, P
SMART; SM
PROSITE;
PROSITE;
                                                                                                                         VCA1_HUMAN
P19320;
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DOMAIN
                                                                                                                                                 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Class II genes of miniature swine. IV. expression of two allelic class II DQB J. Immunol. 145:1946-1951(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1.
Pfam; PF00969; WHC II beta; 1.
Probom; PD000328; MHC II beta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sache D.
                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHC II; Transmembrane; Glycoprotein; Signal. SIGNAL 1 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M31498; AAA31085.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00353; MHC_II_beta.
                                                      VCAM1 OR LICAM
                                          iomo sapiens
                                                                                                                                                                                             173
                                                                                                                                                                                                                                          113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P13760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00407; IGc1; 1.
E; PS50835; IG_LIKE; 1.
E; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                               SKAKG----QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN-NYK
                                                                                                                                                                                                                                                                                                            WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
                                                                                                                                                                                            STPLIRNGD---WTYQVLVMLEMNLQRGDVYTCRVEHSSLQS
                                                                                                                                                                                                                  TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN
                                                                                                                                                                                                                                          QIEEGTTLQRRVQPTVTISPSKAEALNHHNLLVCAVTDFYPSQVKVQWFRNGQEETAGVV
                                                                                                                                                                                                                                                                                      WSVDRY-IYNQEEFLRFDSDMGEYRAVTPLGRPDADYLNGQKEALEQKRAELDTVCKHNY
                                                                                                                                                                                                                                                                                                                                                                               146
48
258
                                                                                    (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  32
124
218
228
249
                                                                                                                                                                                                                                                                                                                                     Conservative
                                           (Human)
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                                                                                                                                     STANDARD;
                    Chordata;
Primates;
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217
227
248
258
108
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                                                                            protein
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                                                                                                                                                                                                                                                                                                                                              Score 161; DB 1;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQ HAPLOTYPE D BETA C EXTRACELLULAR BETA-1. EXTRACELLULAR BETA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLA CLASS II HISTOCOMPATIBILITY DQ HAPLOTYPE D BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONNECTING
                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                 E3AC75110AED47C3
                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                            precursor
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                                                                                                                                     739
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                                                                            (V-CAM
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                                                                                                                                                                                                                                                                                                                                                        Length 258;
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                                                                                                                                                                                             211
                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                            (CD106 antigen)
                                                                                                                                                                                                                                                                                                                                    8
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RC TISSUE-Retinal pigment epithellum;

RX MEDLINE-22388257; PubMede-12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechnic L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Altein D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Altein D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mhting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

"Generation and initial analysis of more than 15,000 full-length

"Thuman and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91352090; PubMed=1715583;
Cybulaky M.I., Fries J.W.U., Williams A.J., Sulta
Byers M., Shows T., Gimbrone M.A. Jr., Collins T.
Byers M., Shows T., Gimbrone M.A. Jr., Collins T.
"Gene structure, chromosomal location, and basis
splicing of the human VCAM1 gene.";
Proc. Natl. Acad. Sci. U.S.A. 88:7859-7863(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rajkumar N.R., Toth E.J., Submitted (AUG-2002) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91201302; PubMed=1707873;
Hession C., Tizard R., Vassallo C., Schiffer S.B., Goff D., Moy P.
Chi-Rosso G., Luhowskyj S., Lobb R., Osborn L.;
"Cloning of an alternate form of vascular cell adhesion molecule-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Direct expression cloning of vascular cell adhesion molecule 1, cytokine-induced endothelial protein that binds to lymphocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRBLINE=91016951; PubMed=1699207;
Polte T., Newman W., Gopal T.V.;
"Full length vascular cell adhesion molecule 1 (VCAM-1).";
Nucleic Acids Res. 18:5901-5901(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE=Umbilical vein;
                                                                       Edwards R.M., Clements J.M., Dudgeon T.J., Stuart D.I. "Crystal structure of an integrin-binding fragment of adhesion molecule-1 at 1.8-A resolution.";
Vature 373:539-544(1995).
                                                                                                                                                         MEDLINE=95147978; PubMe
Jones E.Y., Harlos K.,
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                                 MEDLINE=95296382; PubMed=7539925;
                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS)
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                                                    K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS)
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Pepinsky R.B.,
Osborn L.;
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Toth E.J., Yi Q., Nickerson
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                                                                                                                                                                              PubMed=7531291;
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n C., Tizard R.,
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                  Stehle
                Τ.,
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                Liu J.-H.,
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PIR; A41288; A41288.

PIR; B41288; B41288.

PDB; 1VCA; 15-SEP-95.

PDB; 1VSC; 20-JUN-96.

PDB; 11J9; 07-NOV-01.

Genew; HGNC:12663; VCAM1.
                                         Pram; PF00047; ig; 6.

PRINTS; PR01472; ICAMVCAM1.

PRINTS; PR01474; VCAM1.

SMART; SM00408; IGc2; 3.

PROSITE; PS50835; IG_LIKE; 5.

Immunoglobulin domain; Glycoprotein; Cell adhesion; Repeat; Signal; Alternative splicing; Polymorphism; REPARTY.

PROBABLE PROBABLE
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                                                                                                                                                         InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-1ke.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003989; VCAM-1.
Pfam; PF00047; ig; 6.
                                                                                                                                                                                                                                                                                                                                                    EMBL; X53051; CAA37218.1; -.
EMBL; M30257; AAA61917.1; ALT_TERM.
EMBL; M73255; AAA61270.1; -.
EMBL; M60335; AAA61269.1; -.
EMBL; AF536818; AAM96190.1; -.
EMBL; BC017276; AAH17276.1; -.
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                                                                                                                                                                                                                                           MIM; 192225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as low modified and this statement is not remove entitles requires a license agreement (s) or send an email to license@isb-sib.ch).
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Osborn L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The crystal structure of an N-terminal two-domain fragment of vascular cell adhesion molecule 1 (VCAM-1): a cyclic peptide based the domain 1 C-D loop can inhibit VCAM-1-alpha 4 integrin interaction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure of a functional fragment of VCAM-1 refined at 1.9-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Sialoglycoprotein.

DISEASE: May play an important role in the genesis o artherosclerosis and rheumatoid arthritis.

SIMILARITY: Contains 7 immunoglobulin-like C2-type di DATABASE: NAME=PROW; NOTE=CD guide CD106 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd106.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         well as on macrophage-like and and inflamed tissue.
INDUCTION: P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a Crystallogr. D 52:369-379(1996).

EUNCTION: IMPORTANT IN CELL-CELL RECOGNITION. APPEARS TO FUNCTION IN LEUKOCYTE-ENDOTHELIAL CELL ADHESION. INTERACTS WITH THE BETA-1 INTEGRIN VLA4 ON LEUKOCYTES, AND MEDIATES BOTH ADHESION AND SIGNAL TRANSDUCTION. THE VCAM1/VLA4 INTERACTION MAY PLAY A PATHOPHYSIOLOGIC ROLLS BOTH IN IMMUNE RESPONSES AND IN LEUKOCYTE EMIGRATION TO SITES OF INFLAWMATION.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European
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ISSUE SPECIFICITY: Expressed on inflamed vascular endothelium, as
il as on macrophage-like and dendritic cell types in both normal
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Pepinsky R.B.,
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               VASCULAR CELL
EXTRACELLULAR
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Liu J.-H., Karpusas
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                                          CPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
                                                        APEIFWSKKLDNGNLQHLSGNATLTLIAMRMEDSGIYVCEGVNLIGKNRKEVELIVQ---
                                                                      SPSV----QCRSPRGKNIQGGKTLSVSQLELQDSGTWTC----TVLQNQKKVEFKIDIVP
                                                                                     LVCRAKLHIDEMDSVPTVRQAVKĖLQVYISPKNTVISVNPSTKLQEGGSVTMTCSSEGLP
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bred. No. 203;
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
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                          Pfam; PF00041; fn3; Pfam; PF00047; ig; (PF00047; FN')
                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMI
                                                                                                                                                                      EMBL; X89204; CAA61490.1; -. PIR; T30581; T30581.
HSSP; P20241; 1CFB.
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Actinopterygii; Neopterygii; Teleostei;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neural cell
                                                                      ZFIN; ZDB-GENE-980526-512; nadll.1.
InterPro; IPR008957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR003962; FnIII subd.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurosci. Res. 42:547-561(1995)
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TISSUE=Embryo;
                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                axonogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tongiorgi E., Bernhardt R.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Cell adhesion molecule with an important role in the development of the nervous system. Involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc. Binds to exonin on neurons (By similarity).

SUBCELCULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: Expressed in postmitotic neurones in 16-36 hour embryos, including those in the brain, cranial ganglia and
                                                                                                                                                                                                                                                                                                                                                         initiation of axonogenesis in 16-36 hour embryos.
SIMILARITY: Belongs to the immunoglobulin superfamily.
Ll/neurofascin/NgCAM family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: Onset of expression correlates with initiation of axonogenesis in 16-36 hour embryos.
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                                                                                                                                                                                                                                   email to license@isb-sib.ch).
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(Rel. 42, Last sequence update)
(Rel. 43, Last annotation update)
adhesion molecule L1.1 (N-CAM L1.1)
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Ostariophysi; Cypriniform
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PROSITE; PS50835; IG LIKE; 6.

Neurogenesis; Cell adhesion; Developmental protein; Glycoprotein;
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                                                                                    IEGSLKVLDVQMEDM---GIYSCEVST-TLDSDTASGYITVQDKPDPPQSLKLSEKMER-
                                                                                                        TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDEL
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FIBRONECTIN TYPE-III 2
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FIBRONECTIN TYPE-III 5
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IG-LIKE C2-TYPE 6
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IG-LIKE C2-TYPE 6
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4; Mismatches
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                                                          MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A
"Characterization of the two uniq
                                                                                                                         Biochemistry
                                                                                                                                                          PARTIAL SEQUENCE (MYELOMA PROTEIN MEDLINE=74109253; PubMed=4814727; Chen B.L., Poljak R.J.;
                                                                                                                                                                                                                                "Structural rule of antibodies. Primary structure of a immunoglobulin-L-chain of the lambda type, subgroup IV protein Kern). V. The complete amino acid sequence and
                                                                                                                                                                                                                                                                                  SEQUENCE (BENCE-JONES PROTEIN KERN).
MEDLINE=71150336; PubMed=5549568;
                                                                                                                                                                                                                                                                                                                                                                                                                       Bence-Jones protein.";
Biochem. J. 110:631-652(1968)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
  MEDLINE=75046825;
              X-RAY CRYSTALLOGRAPHY
                                                                                                  SEQUENCE (DOT)
                                                                                                                      "Amino acid sequence of the (lambda) immunoglobulin (IgG New)."; Biochemistry 13:1295-1302(1974).
                                                                                                                                                                                                                                                                        Ponstingl H.,
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (BENCE-JONES PROTEIN NIG-64).
MEDLINE=83186114; PubMed=6404900;
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"Immunoglobulin lambda-chains. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=69088380; PubMed=4883841
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                                                                                                                                                                                                                                                                                                                      'Comparative studies on the structure of the light chains of mmunoglobulins. IV. Assignment of a subsubgroup."; Biochem. 93:421-429(1983).
                                                                                                                                                                                                                         nterpretation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENCE (BENCE-JONES PROTEIN SH).
INE-70166723; PubMed=4909564;
ni K., Wikler M., Shinoda T., Put
amino acid sequence of a lambda
lete amino acid sequence and the
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                                     228:886-893 (1995)
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yasu T., Suzuki
PubMed=4215080;
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Genew; HGNC:5 Genew; HGNC:5 Genew; HGNC:5 MIM; 147220;

HGNC:5855; IGLC1. HGNC:5856; IGLC2. HGNC:5857; IGLC3.

GO; GO:0003823; F:antigen binding; GO; GO:0006955; P:immune response; InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig-Cl.
InterPro; IPR003006; Ig_MHC.

Pfam; PF00047; ig; 1. SMART; SM00407; IGc1; 1

PS50835; IG_LIKE; 1.

EMBL; PIR; /

15-JUL-92. 31-JAN-94. 15-MAY-97 04-FEB-98.

L2HU.

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EMBL; J00253; AAA59107.1;
EMBL; L38562; AAB36581.1; A
EMBL; X51754; CAB38659.1; A
EMBL; X51755; CAA36049.1;
EMBL; X51755; CAA36051.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (11)
SEQUENCE FROM N.A.
MEDLINE-82080680; PubMed=6273747;
Hieter P.A., Hollis G.F., Korsmey
APTRAGEMENT Of immunog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY OF MCG. MEDILINE=90133913; PubMed=2515285; Ely K.R., Herron J.N., Harker M., "Three-dimensional structure of a water. Conformational flexibility
                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced throu between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no reuse by non-profit institutions as long as its contenmodified and this statement is not removed. Usage by
                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 294:536-540(1981).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.3 Edmundson A.B., Ely K.R., A Panagiotopoulos N.; "Rotational allomerism and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The three-dimensional myeloma immunoglobulin Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in man."
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Saul F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                              found in proteins SH, X, and NIG-64. The Kern protein has the Kern+ marker, the NEWM protein has the Oz+ marker, the Mcg protein has the Kern+ marker, and the Mcg+ marker and the Mcg+ marker.

MISCELLANEOUS: Six tandem lambda-type genes were identified and the 3 most 5' were sequenced. These correspond to the Mcg sequenced. These correspond to the Mcg sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                      sequence (lambda-3).
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=75013804; PubMed=4415202;
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at 2.0-A resolution.";
U.S.A. 71:3440-3444(1974).
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light chain dimer
of a molecule in t
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The Kern protein h
he Oz+ marker, the |
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Fujioka Y., Kasug
"Mouse and human
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localization of genes.";
Biochem. Biophys. Res. C
[2]
                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation type substrate 1 precent types in the protein-tyrosine phosphatase non-receptor type substrate 1 precent (SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signa-1) (S
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P78324; 000683;
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                                                                                          MEDLINE=97223399; PubMed=9070220;
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FISSUE=Brain;
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105
                                                       Kasuga M.;
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; 043799; Q8NS17;
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OR MYD1 OR BIT OR MFR.
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Pred. No. 0.
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R -> K (IN OZ+ MARKER).
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S -> G (IN KERN+ MARKER).
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7; Q8TAL8; '
                 231:61-67 (1997)
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Q9H0Z2;
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RA Deloukas P., Matthews L.H., Abhurst J., Burton J., Gilbert J.G.R., And Deloukas P., Matthews G., Almeida J.P., Babbage A.K., Bagguley C.L., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Chegy S., Cobley V.E., Collier R.E., Comnor R.E., Corby N.R., RA Clegy S., Cobley V.E., Collier R.E., Comnor R.E., Corby N.R., RA Clegy S., Cobley V.E., Collier R.E., Comnor R.E., Corby N.R., RA Clegy S., Cobley V.E., Collier R.E., Comnor R.E., Corby N.R., RA Clegy S., Cobley V.E., Griffiths M.N.D., Gwilliam R., Hall R.E., RA Hummond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J., RA Hummond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howden P.J., RA Hummond S., Harley J.L., Heath P.D., HO S., Holden J.L., Howlen P.J., RA Lehvaslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H., RA Swune R.M., Sycamore N., Taylor R., Febra H.K., Shownkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Febra H.K., Shownkeen R., Sims S., Swann R.M., Sycamore N., Taylor R., Febra H.K., Shownkeen R., Sims S., RA Wilhelm S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., RA Wilhiang L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., RA Milne S.J., Williams S.A., Milne S.J., Williams S.A., RA Williams J., Williams S.A., Beck S.,
          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS LEU-44; TP
THR-52; ARG-54; ALA-57; GLY-75; ASP-95; LEU-96; ASN-100; ARG-
PGLY-109 AND VAL-131.

TISSUE-Brain, Kidney, and Skin;

X MEDLINE=22388257; PubMed=12477932;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler

A Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N

A Rischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heigh F

A Hopkins R.F., Jordan H., Moore T., Max S., Carnin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schee

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prang
                                                                                                                                                                                                                                                                                                    Rogers
"The D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brooke G.P., Parsons K.R., Howard C.J.;
"Cloning of two members of the SIRP alpha family of protein tyros
phosphatase binding proteins in cattle that are expressed on mono
and a subpopulation of dendritic cells and which mediate binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Monocytes;
MEDLINE=98143722; PubMed=9485180;
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                                                                                                                                                                                                                                                                                 DNA sequence and comparative re 414:865-871(2001).
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e structure
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Loquellano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; PubMed=10585853;
ishi H., Kubota M.;
of mouse BIT/SHPS-1.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9062191;
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Y-75; ASP-95;
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ND INTERACTIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND VARIANTS LEU-44; THR-50; THR-52; LEU-96; ASN-100; ARG-107; GLY-109 AN
                                                                                                                                                                                                                                                                                                    analysis of
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                                                                                                                 .H., Derge J.G.,
Shenmen C.M., Schuler
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                                                                                                                                                                                                                                                                                                      human
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                                                                        F., Bhat N.K.,
J., Hsieh F.,
                                                                                                                                                                                                                                                                                                      chromosome 20.";
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                    Scheetz T.E.,
Prange C.,
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  Mullahy
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monocytes
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J. Immunol. 167:2547-2554(2001).

-i- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts as docking protein and induces translocation of PTPN6, PTPN11 and other binding partners from the cycosol to the plasma membrane. Supports adhesion of cerebellar neurons, neurite outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synaptic function (By similarity). Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell adhesion, growth factors or insulin. Mediates negative regulation of phagocytosis, mast cell activation and dendritic cell activation. CD47 binding prevents maturation of immature dendritic cells and inhibits cytokine production by mature dendritic cells.

-I- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro. Binds FGR (By similarity). Binds JAK2 irrespective of its phosphorylation status and forms a stable complex. Binds SCAP1 and/or SCAP2. The resulting complex recruits FYB. Binds PTKZB.

-I- ALTERNATIVE PRODUCTS:

Eventella resulting complex recruits FYB. Binds PTKZB.

FLYANTENATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.F. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanches Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Delespesse G., Sarfati M., "Bidirectional negative regulation of human T and dendritic combined the cognate receptor signal-regulator protein-alpha: down-regulation of IL-12 responsiveness and inhibition of dencell activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION BY JAK2, AND INTERACTIO MEDLINE=20428742; Pubmed=10842184; Stofega M.R., Argetsinger L.S., Wang H. "Negative regulation of growth hormone signal regulatory protein alpha."; J. Biol. Chem. 275:28222-28229(2000).
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Latour S., Tanaka H., Demeure C., Mateo V., Rubio M.,
Maliezewski C., Lindberg F.P., Oldenborg A., Ullrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multi-protein complexes in macrophages.";
Curr. Biol. 9:927-930(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION, AND INTERACTION WITH CD47.
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                   pancreas.
PTM: N-gl
                                                                                                 Note=No experimental conf
TISSUE SPECIFICITY: Ubiquit
Detected on myeloid cells,
                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=3;
                                                                              levels in heart,
                                                                                                                                                                                                      Note=No
                                                                                                                                                              IsoId=P78324-3; Sequence=VSP_007029;
                                                                                                                                                                                                      Good=P78324-2; Sequence=VSP_007030;
Gote=No experimental confirmation av
                                                                                                                                                                                                                                                                 [soId=P78324-1;
Phosphorylated
                     N-glycosylated
                                                           intestine,
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                                                         placenta, prostate,
                                                                                                                                                                                                                                                                 Sequence=Displayed;
                                                    tal confirmation available;

Ubiquitous. Highly expressed in brain.

Cells, but not T cells. Detected at lower
acenta, lung, testis, ovary, colon, liver,
ostate, spleen, kidney, skeletal muscle an
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tyrosine residues
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                                                                                                                                                                                                      available,
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'n
response
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, Gibbs R.A.,
igues S
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signaling
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Best Local 9
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                                                                                                                                                    LAC PIG
P01846;
                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
11 lambda chain C region.
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                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                        NCBI_TaxID=9823;
                                                                                  Sus scrofa (Pig)
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PIR; JC5287; JC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stimulation with EGF, growth hormone, insul
Dephosphorylated by PTPN11.
-i- SIMILARITY: Contains 2 immunoglobulin-like
-i- SIMILARITY: Contains 1 immunoglobulin-like
MEDLINE=78000254; PubMed=409425
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005886; C:plasma membrane; TAS
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                                                                                                                                                                                                                                                                   423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALI034562; CAB38874.1; -.
ALI049634; CAB46662.1; ALT_SEQ.
ALI17335; CAC12723.1; -.
BC026692; AAH26692.1; -.
BC033092; AAH33092.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D86043; BAA12974.1; -.
Y10375; CAA71403.1; -.
Y11047; CAA71944.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB023430; BAA87929.1;
AC004832; AAF19260.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGNC:9662; PTPNS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                        LK-VSAHPKEQGSNTAAE
                                                                                                                                                                                                                                                                   QKSLSLSPGLQLDETCAE 440
                                                                                                                                                                                                                                                                                                                                                                                                                                  DPEVKFNWYVDGVEVHNAKTK--PREE----QYNSTYRVVSVLTVLHQDWLNGKEYKCKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVL-QNQKKVE
                                                                                                                                                                                                                                                                                                                                                                             SNKALPA-PIEKT--ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                                                                                                                                                                                                          D--ITLKWFKNGNELSDFQTNVDPVGESVSYSIHSTAKVVLTREDVHSQVI-----CEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FK----SGAGTELSVRAKPSAP-VVSGPAARATP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPARELIYNQKEGHFPRVTTVSESTKRENMDFSISISNITPADAGTYYCVKFRKGSPDTE
                                                                                                                                                                                                                                                                                             WLENGNVSRTETASTVTENKDGTYNWMSWLLVNVSAHRDDVKLTCQVEHDGQPAVSKSHD
                                                                                                                                                                                                                                                                                                                       WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE---ALHNHYT
                                                                                                                                                                                                                                                                                                                                                   AHVTLQGDPLRGTANLSETIRVPPTLEV-TQQPVRAE---NQVNVTCQVRKFYPQRLQLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.8%;
ilarity 24.8%;
Conservative 4
                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH38510.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 156.5; DB Pred. No. 0.0069; S; Mismatches 15
                                                                                                                                                                   PRT;
                                                                                                                                                                    105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce,
                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin and
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V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                        Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QHTVSFTCESHGFSPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 81
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Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACS_N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
                          InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 1.
SMART; SM00407; IGc1; 1.
                                                                                             EMBL; M35582;
HSSP; P01842;
                                                                                                                                                                                                                                                    Mami F., Cazenave P.A., Kindt T.J.; "Conservation of the immunoglobulin C lambda 5 gene in the EMBO J. 7:117-122(1988).
                                                                                                                                                                                                                                                                                                                                              Mus spretus (Western wild mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1991
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                 P20765;
01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A02129; L1PG.
HSSP; P01842; 2MCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochemistry 16:3765-3772 (1977)
                                                                                                                                                                                                                                                                                 MEDLINE=88196070; PubMed=3129289;
Mami F., Cazenave P.A., Kindt T.J
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novotny J., Franek F., Margolies M.N., Haber E., "Amino acid sequence of normal (microheterogeneo
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10096;
                                                                                                                                                                                                                                                                                                                                                                                         Ig lambda-5 chain C region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR007110; Ig-like.
nterPro; IPR003597; Ig_cl.
nterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                          SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISCELLANEOUS: This chain was obtained from a mixture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobuling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASSUM
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M00407; IGC1; 1.
PS50835; IG_LIKE; 1.
PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNNKYAASSYLALSASDWKSSSGFTCQVTHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPKAAPTVNLFPPSSEELGTNKATLVCLISDFYPGAVTVTWKAGGTTVTQGVETTKPSKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27
104
                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 17, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                         AAA39152.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain; Immunoglobulin C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lambda chains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11003 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.8%;
35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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; 3817AAEBD747C396 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 156;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
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                                                                                                                                                                                                                                                                   gene.";
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RESULT 82
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                                                                                                  Query Match
Best Local S
Matches 32
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Best Local (
                                                                                                                                                  DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                             Přam; Př00047; ig; 1.
SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin domain; Immunoglobulin C region.

NON TER 1 1

DOMĀIN 6 100 IG-LIKE.

DISULPID 27 86

DISULPID 27 86

DISULPID 104 104 INTERCHAIN (WITH FEQUENCE 105 AA; 11674 MW; AAB417DF68471A17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAC_RABIT P01847;
                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin lambda-chains.
Biochem. J. 197:177-183(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel.
01-FEB-1991 (Rel.
10-OCT-2003 (Rel.
                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                     PIR; A02130; L7RB.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                            Garcia I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82091105; PubMed=6797414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                     Immunoglobulin
                                                                                                                                                                                                                                                                                                                                              specificity.
-!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig lambda chain C region.

    -!- MISCELLANEOUS: This lambda chain expresses the c7 allotypic

                                                                                                                                                                                                                                                                                                                                                                                                             The primary structure of the constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385
                        390
9
                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TNNKYMVSSYLTLISDQWMPHSRYSCRVTHE---GNTVEKSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                  σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                              PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLDSDGSF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
                        FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QPKSDPLVTLFLPSLKNLQANKVTLVCLVSEFYPGTLVVDWKVDGVPVTQGVETTQPSKQ 60
AASSFLHLTANQWKSYQSVTCQVTHE---GHTVEKSLA 100
                                                  PSVILFPPSSEELKDNKATLVCLISDFYPRTVKVNWKADGNSVTQGVDTTQPSKQSNNKY
                                                                                                                                                                                                                                                                                                                                                                                        J. 197:177-183(1981)
                                                                                                                                                     105
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01,
17,
42,
                                                                                                                                                    11484 MW;
                                                                                                             5.7%;
32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                    17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 153.5; |
Pred. No. 0.00
20; Mismatches
                                                                                                  Score 153; DB
Pred. No. 0.00
17; Mismatches
                                                                                                                                                    INTERCHAIN (WITH HEAVY CHAIN).; B427513272E8663D CRC64;
                                                                                                                                                                                        IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (WITH HEAVY CHAIN)
AAB417DF68471A17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105
                                                                                                                                                                                                                    a
                                                                                                                                                                                                                  region
                                                                                                              DB 1; Length 105 .0016;
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                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                              of Basilea-rabbit
                                                                                                                                                                                                                                                                                                                                                 domain
                         427
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                                                  65
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RESULT 83 KACB_RABIT

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RESULT
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Best Local S
Matches 31
                                                                     CEA5 HUMAN
P06731;
01-JAN-1988
                                                                                                                                                                                                                                                                                                    DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Multiplicity of constant kappa light chain genome: a b4b4 homozygous rabbit contains a EMBO J. 2:437-441(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986
21-JUL-1986
15-MAR-2004
                                                                                                           HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; FALSE NEG.
Immunoglobulin domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGcl; 1.
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Mammalia; Eutheria;
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K-BAS
                                   Carcinoembryonic
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                     (Carcinoembryonic
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is lambda. The kappa chain shown is
rabbit B allotypes have Cys-64.
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004 (Rel. 43, Last anno-
ronic antigen-related c
antigen) (CEA)
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                                                                                                                                                                               VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 413
                                                                                                                                                                                                       GDPVAPSVLLFPPSKEELTTGTATIVCVANKFYPSDITVTWKVDGTTQQSGIENSKT--P
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
utheria; Lagomorpha; Leporidae; Oryctolagus.
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Last annotation update;
gen-related cell adhesion molecule
igen) (CEA) (Meconium antigen 100)
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Mammalia; Eutheri
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MEDINE=87128144; PubMed=3814146;
Olkawa S., Nakazato H., Kosaki G.;
"Primary structure of human carcinoembryonic antigen from cDNA sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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Zimmermann W., Ortlieb B., Friedrich R., von Kleist
"Isolation and characterization of cDNA clones encoc
carcinoembryonic antigen reveal a highly conserved :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89122014; PubMed=3220478; Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.; Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.; Characterization of cDNAs "Carcinoembryonic antigen family: characterization of cDNAs for NCA and CEA and suggestion of nonrandom sequence variation of conserved loop-domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beauchemin N., Benchimol S., Cournoyer D., Fuks "Isolation and characterization of full-length for human carcinoembryonic antigen."; mol. Cell. Biol. 7:3221-3230(1987).
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Hassauer M., Shively
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 331-702 FROM
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SIMILARITY: Belongs to the immunoglobulin superfamily. SIMILARITY: Contains 7 immunoglobulin-like domains. DATABASE: NAME-PROW; NOTE-CD guide CD66e entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd66e.htm".
        M17303;
M592562;
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62; AAA62835.1; ALT SEQ.
55; AAA62835.1; JOINED.
57; AAA62835.1; JOINED.
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EMBL; M16234; AAA51972.1; -.
PIR; A36319; A36319.
PDB; 1807; 04-JUL-00.
Genow; HGNC:1817; CEACAMS.
MIM; 114890; -.
GO; GO:0005887; C:integral to pl
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Pfam, PP0047; ig, 6.
PROSITE, PS50835; IG_LIKE; 6.
Immunoglobulin domain; Glycoprotein; Lipoprotein; GPT-anchor;
Immunoglobulin domain; Glycoprotein; GPT-anchor;
Immunoglobulin domain; Glycoprotein; Lipoprotein; GPT-anchor;
Immunoglobulin domain; Glycoprotein; GPT-anchor;
Immunoglobulin domain; Glycoprotein; GPT-anchor;
Immunoglobulin domain; GPT-
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 178
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                                                                                                                                                                                                                  Similarity
DSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM
                                                                                   QELFIPNITVNNSGSYTCOAH------NSDTGLNRTTVTTITVYAEPPKPF
                                                                                                                                              RSGENLNLSCHAASNPPAQYSWFVN--
                                                                                                                                                                        KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGN
                           ITSNNSNPVEDEDAVALTCEPEIQNTTYLWWVNNQSLPVSPRLQLSNDNRTLTLLSVTRN
                                                                                                                FPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP----
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                  18.0%;
                                                                                                                                                                                                                                                              76795 MW;
                                                        -SVQCR---
                                                                                                                                                                                                     78;
                                                                                                                                                                                                     Score 151.5;
Pred. No. 0.02
78; Mismatches
                                                                                                                                                                                                                                                                            N-LINKED
MISSING (
                                                                                                                                                                                                                                                                                                      N-LINKED
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IG-LIKE 2.
IG-LIKE 3.
IG-LIKE 4.
IG-LIKE 5.
IG-LIKE 6.
IG-LIKE 7.
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REMOVED IN MATURE FORM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasma membrane; TAS
                                                                                                                                                                                                                                                              6299AE26CDDBDB5C CRC64;
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RESULT 85
KACA_RAT
ID KACA
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                                                                                       Query Match
Best Local S
Matches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PO1836;
21-UUL-1986 (Rel. 01, Createu,
21-UUL-1986 (Rel. 01, Last sequence up)
10-CCT-2003 (Rel. 42, Last annotation
"- ranna chain C region, A allele."
"- ranna chain C region, A allele."
                                                                                                                                                                                DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                Immunoglobulin
NON TER 1
DOMAIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                  PFAMT, PF00047; ig; 1.
SMART; SM00407; IGC1; I.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A02118; K1RTA.
HSSP; P01842; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=82082587; PubMed=6273908;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KACA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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                                                                                                              Similarity
                         PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DKDAVAFTCEPEA---QNTTYLWWVNGQ----SLPVSPRLQLSNGN----RTLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNITEKNSGLYTCQANNSASGHSRTTVKTITVSAELPKP---SISSNNSKPVE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISRT---PEVTCVVVDVSHEDPEVKFNWYVDG-VEVHNAKTKPREEQYNSTYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVGPYECGI-QNELSVD---
PTVSIFPPSMEQLTSGGATVVCFVNNFYPRDISVKWKIDGSEQRD-----GVLDSVTDQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSASGTSPGLS----AGATVGIMIGVLVGVALI 702
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                                                                                                                                                                                   106 AA;
                                                                                                                                                                                                      26
106
                                                                                                                                                                                                                                                                                               domain; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                          5.6%;
31.5%;
                                                                                                                                                                                   11732 MW;
                                                                                       Score 150; DB
Pred. No. 0.00
23; Mismatches
                                                                                                                                                                                INTERCHAIN (WITH A B7E120D9700DDD66
                                                                                                                                                                                                                                                  IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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on update)
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                                                                                                                                                                                                          HEAVY CHAIN)
                                                                                                                                    Length
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  59
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Best Local S
Matches 56
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Pfam; PF00969; MHC II beta; 1.
ProDom; PD000328; MHC: II beta;
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                           DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990
01-APR-1990
15-JUL-1999
                                                                                                                                                                         TRANSMEM
DOMAIN
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98 LT
                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90361905; PubMed=2391424;
MEDLINE=90361905; PubMed=2391424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HB2C_PI
P15982;
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000333; MHC_II_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M31497; AAA31084.1; -. EMBL; M32117; AAA53110.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sache D.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursor.
Sus scrofa (Pig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
SLA class II histocompatibility antigen, DQ haplotype C beta chain
                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P13760;
                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A60404; A60404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Class II genes of miniature swine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunol. 145:1946-1951(1990)
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            240
                                                        180
                                   12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                          Similarity
                                                                                                                                                                                                                                                                    Transmembrane;
         RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWL
                                GLWTAAL-----TVMLVVLGAPVAEGRD-----SPQDFVFQFK-GECYFYN
                                                       GTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKDSTYSMSSTLSLTKVEYERHNLYTCEVVHK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- DGSFFLYSKLTVDKSRWQQGNVFSCSVMHE 415
                                                                                                                                        32
127
221
231
252
252
149
149
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(Rel.
                                                                               Conservative
                                                                                                                            Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                  126
220
230
251
261
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205
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Cetartiodactyla; Suina;
::
                                                                                                                            29550
                                                                                          5.5%;
23.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                  Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                             I_beta; 1.
                                                                                                                            MW;
                                                                               40;
                                                                                                                                                                                                       DQ HAPLOTYPE C BETA C EXTRACELLULAR BETA-1. EXTRACELLULAR BETA-2.
                                                                              Pred. No. 0.0
); Mismatches
                                                                                          Score 149.5;
Pred. No. 0.0
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RESULT 87
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9270J8
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                   Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institu modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-I-TISSUE SPECIFICITY: Highly expressed in brain.
-i- PTM: GlyCosylated.
-i- SIMILARITY: Belongs to the immunoglobulin superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- FUNCTION: CELL-ADHESION (POTENTIAL).
-1- SUBCELLULAR LOCATION: Attached to the membrane
-1- TISSUB SPECIFICITY: Highly expressed in brain.
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    CARBOHYD
                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 3.
SMART; SM00408; IGc2; 2
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; InterPro; IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB017139; BAA75649.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF MEDLINE=99175207; PubMed=10075727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                       mmunoglobulin domain;
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
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the IgLON cell adhesion molecule
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CARBOHYD
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P01834;
                                                                                Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones proter). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
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21-JUL-1986 (Rel. 01,
15-MAR-2004 (Rel. 43,
                    SEQUENCE FROM N.A. MEDLINE-81042304;
                                                                                                                                                                                                                                                                                    Biochemistry
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                   "The covalent structure of a human Intrachain disulfide bonds.";
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=71064027; PubMed=4923144;
                                                                                                                                                                                                                                                                                                                                                                                           DISULFIDE BONDS.
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  Max E.E.,
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                      PubMed=6775818,
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Pred. No. 0.013;
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  J.G.,
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-LINKED (GLCNAC. . .) (POTENTIAL)
37E90D1C7D24ACAB CRC64;
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nan gamma G-immunoglobulin. VI.
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InterPro; IPR007110; Ig-like InterPro; IPR003597; Ig c1. InterPro; IPR00306; Ig_MHC. Pfam; PF00047; Ig; 1. SMART; SM00407; IGc1; 1.

PS50835;

IG_LIKE; 1

GO:0003823; F:antigen binding; GO:0006955; P:immune response;

Genew;

HGNC:5716;

IGKC

08-AUG-01. 15-MAY-97.

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Olsen K.E., Sletten K., Westermark P.;
"Extended analysis of AL-amyloid protein from abdominal wall subcutaneous fat biopsy: kappa IV immunoglobulin light chain Biochem. Biophys. Res. Commun. 245:713-716(1998).
-I- MISCELLANEOUS: The EU sequence has the INV (3) allotypic 45-Ala and 83-Val. The ROY sequence has the INV (1,2) all marker, 45-Ala and 83-Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H118Chmann N., Barnikol H.U.,
Steinmetz-Kayne M., Suter L.,
(In) Franck F., Shugar D. (eds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The
                                                                                                                                                                                                                        EMBL; J00241; AAA58989.1;
EMBL; V00557; CAA23823.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98249779; PubMed=9588180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-33; 38-41 AND TISSUE=Abdominal adipose tip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=70201507; PubMed=5447531;
Kohler H., Shimizu A., Paul C., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=69234734; PubMed=4893682; Titani K., Shinoda T., Putnam F.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 22:197-207(1980)
                                                                                                                                                                                                                                                                                                                                This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Macroglobulin structure:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=68242259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE (BENCE-JONES PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cloned human and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE (BENCE-JONES
                                                                                                                                                ; 1D5B; 09-FEB-00.
; 1D5I; 09-FEB-00.
; 1D6V; 04-OCT-00.
; 1HEZ; 18-JUL-03.
; 1HKL; 12-MAR-97.
                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid sequence of a kappa type Bence-Jones lete sequence and the location of the disulfide kiol. Chem. 244:3550-3560(1969).
                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produce the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete amino acid
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in functional segments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chem. 348:1718-1722(1967).
                                                                                                                                                                                                                                                                    agreement (See http://www.isb-sib.ch/announce,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AG).
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S.;
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Best Local
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                                                                                                                                                                                      Hassel B., Rathjen F.G., Volkmer H.;

"Organization of the neurofascin gene and analysis of developmenta regulated alternative splicing.";

J. Biol. Chem. 272:28742-28749 [1997).
-!- FUNCTION: Cell adhesion, ankyrin-binding protein which may be involved in neurite extension, axonal guidance, synaptogenesis myelination and neuron-glial cell interactions (By similarity)
-!- SUBCELIULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment-A number of isoforms are produced;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98019255; PubMed=9353344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              superfamily.";
J. Cell Biol. 118:149-161(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92317154; PubMed=1377696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; I
Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurofascin
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NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE FROM N.A.
DEVELOPMENTAL STAGE: There is one major 'early' isoform and multiple 'late' isoforms. Around 50 isoforms are found at different developmental stages.

PTM: N-glycosylated and O-glycosylated.

PTM: May be proteolytically cleaved at Arg-636.

SIMILARITY: Belongs to the immunoglobulin superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG--QPENNYKTTPPVLDSDGS
                                                                                                                                                            IsoId=042414-1; Sequence=Displayed;
                                                                                                                         IsoId=042414-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND
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5, CLEAVAGE A
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Weognathae; Galliformes; Phasianidae; Phasianinae;
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/FTId=VAR 003897.
D -> N (IN REF. 7 AND 8).
E -> Q (IN REF. 5 AND 6).
W; 51984D1FDD372CE8 CRC64;
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Pred. No. 0.0034;
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      Pfam; PF00041; fn3; 5.
Pfam; PF00047; ig; 6.
SMART; SM00460; FN3; 5.
SMART; SM00408; IGC2; 3.
SMART; SM00408; IGC2; 3.
PROSITE; PS50835; IG LIKE; 6.
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InterPro; IPR003598;
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SIMILARITY: Contains 5 fibronectin type III domains.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
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X14341; CAA74726.1;

X14342; CAA74726.1;

X14343; CAA74726.1;

X14343; CAA74726.1;

X14344; CAA74726.1;

X14346; CAA74726.1;

X14347; CAA74726.1;

X14348; CAA74726.1;

X14349; CAA74726.1;

X14350; CAA74726.1;

X14350; CAA74726.1;
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; P20241; 1CFB.
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Y14353; CAA74726.1;
Y14354; CAA74726.1;
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FN III-like.
FIG-like.
FIG_C2.
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IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 3
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DT 01.NOV-1997 (Rel. 35, L
DT 10.CT-2003 (Rel. 42, L
DE Limbic system-associate
GN LSAMP OR LAMP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Cho
OC Mammalia; Eutheria; Pri
OX NCBI_TaxID=9606;
RN [1]
RN (1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96235133; PubMe
RA Pimenta A.F., Fischer I
RT "CDNA cloning and struc
RT associated membrane pro
RL Gene 170:189-195(1996).
CC -1- FUNCTION: MEDIATES
CC CONTRIBUTES TO THE
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10-OCT-2003 (Rel. 42, Last sequence up.
Limbic system-associated membrane prot LSAMP OR LAMP.
Homo particular
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                                   SEQUENCE FROM N.A.

MEDLINE-96235133; PubMed-8666243;
Pimenta A.F., Fischer I., Levitt P.;
"CDNA cloning and structural analysis
associated membrane protein (LAMP).";
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  FUNCTION: MEDIATES CONTRIBUTES TO THE
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                                                                                                                                 Chordata;
Primates;
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22.3%;
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  SELECTIVE NEURONAL GROV
GUIDANCE OF DEVELOPING
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SCLSSPV -> F (in isoform 2
/FTId-VSP 008935.
Missing (in isoform 2).
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/FTId=VSP_
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Pred. No.
                                                                                                                                 Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                    PRT;
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protein precursor
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(IN REF. 2)
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  GROWTH AND
PING AXONS A
                                                                                                                                   Hominidae;
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                                                      human limbic-system-
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  AND REMODELING
                                                                                                                                               Euteleostomi;
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                TARGETING
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Best Local S
Matches 75
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SWART; SM00408; IGC2; 2.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Cell ac
Repeat; Signal; Lipoprotein.
SIGNAL 1 28
                                                                                                                                                                                                                                                                               CARBOHYD
CARBOHYD
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CARBOHYD
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                                                                                                                                                                                                                                               SEQUENCE
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InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U41901; AAC50569.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                     LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0007399; P:neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; JC4776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROW OF THE HYPPOCAMPAL MOSSY FIBER PROJECTION (BY SIMILARITY).

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. TISSUE SPECIFICITY: Expressed on limbic neurons and fiber tract as well as in single layers of the superior colliculus, spinal chord and cerebellum.

SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                      182
                                                                                       117
                                                                                                             73
                                                                                                                                   62
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                                                                                                                                                                                                   l Similarity
75; Conser
                                                                                                             AGHD
SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA---KTKPREEQ
                                                                 SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPTGREFEGEEEY
                                                                                                                                LGNQGSFLTKGPSKLNDRA--DSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE---
                                                                                                                                                        LVLLRLLCLLPTGLPVRSVDFNRGTDNITVRQGDTAILRCVLEDKNS-KVAWLNRSGIIF
                                                                                                                                                                           LLIVIQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                      LEILGITREQSGKYECKAANEVSSADVKQVKVTVNYPP-TITESKSNEAT
                                         LSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGP
                                                                                     -EVQLLVFG----LTANSDTHLLQGQSLTLTLESPPGSSPSVQCR--SPRGKNIQGGKT-
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                                                                                                                                                                                                   Score 147; DE
Pred. No. 0.01
19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      REMOVED IN MATURE I
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
                                                                                                                                                                                                                                                                               N-LINKED
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N-LINKED
N-LINKED
N-LINKED
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                                                                                                             -EYSLRIQKVDVYDEGSYTCSVQTQHEPKT
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IG-LIKE

C2-TYPE

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"Expression patterns of L1-family cell recognition molecules L1, CHL1,

"I recam, and neurofascin in the mouse brain.";

I NrCAM, and neurofascin in the mouse brain.";

Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

C -!- FUNCTION: Cell adhesion, ankyrin-binding protein which may be involved in neurite extension, axonal guidance, synaptogenesis,

C myelination and neuron-gilal cell interactions (By similarity).

C -!- SUBUNIT: Probable constituent of a neurofascin/NRCAM/ankyrin G complex. Associates with the sodium channel beta-1 (SCN1B) and beta-3 (SCN1B) subunits (By similarity).

C -!- SUBCELLULAR ICCATION: Type I membrane protein.

C -!- SUBCELLULAR ICCATION: Type I membrane protein.
                                                                                                                                                                              Pfam; PF00041; fn3; 4.
Pfam; PF00047; iq; 6.
SMART; SM00060; FN3; 4.
SMART; SM00409; IG; 6.
SMART; SM00408; IGc2; 6.
PROSITE; PS50835; IG_LIKE; 6
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S_MOUSE

NFAS MOUSE

QB10U3;

15-MAR-2004

15-MAR-2004

15-MAR-2004
                                                                                                                       Glycoprotein.
SIGNAL
CHAIN 2
               TRANSMEM
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                             entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                       DOMAIN
                                                                                                                                                                   Cell adhesion; Repeat; Signal;
                                                                                                                                                                                                                                                                    InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ543322; CAD65849.1; -. MGD; MGI:2442229; D430023G06Rik.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                   InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             tities requires a license agreement (Se send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWED outstation - European Bioinformatics Institute are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 6 immunoglobulin-like C2-type du SIMILARITY: Contains 4 fibronectin type III domains.
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE 1.

IG-LIKE C2-TYPE 2.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 3.

IG-LIKE C2-TYPE 5.
                                                                                                       NEUROFASCIN.
EXTRACELLULAR
                                                                                                                                     POTENTIAL
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                                                                                                       (POTENTIAL).
                                                                                                                                                                 Immunoglobulin domain;
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RESULT 92
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Best Local
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                                                          Q9QZS7;
28-FEB-2003
28-FEB-2003
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CARBOHYD
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CARBOHYD
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DOMAIN
DOMAIN
DOMAIN
             Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                         Nephrin precursor NPHS1 OR NPHN.
                                                                                              NPHN MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                        EP---LOSAPPNPNREVAGDTIIFRDTQISSRA-----VYQCNTSNE
                                                                                                                                                          OPENNYKTTPPVLDSD-
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                                                                                                                                                                                                                                DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                                   IDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPE--VTCVVVDVSHE
                                                                                                                                                                                                                                                                                     PVIFWMSSSMEPITQDKRVSQGHNGDLYFSNVMLQDMQTDYSCNARFHFTHTIQQKNPFT
                                                                                                                                                                                                                                                                                               PSVQCRSPRGKNIQGGKTLS-----VSQLELQDSGT-WTCTVLQN-----
                                                                                                                                                                                                                                                                                                                       ALSNRIRLQVSKSPLW-----PKENLDPVV-------VQEGAPLTLQCNPPPGLPS
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                                                                                                                                                                             GSIRHTISVRVKAAPYWLDEPKNLILAPGEDG
                                                                                                                                                                                                                -PTPDIAWYKKGGDLPSNKAK--FENFNKALRITNVSEE-----DSGEYFCLASNKM--
                                                                                                                                                                                                                                                  LKVLTTRGVAERT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
cursor (Renal glomerulus-specific
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                               (Mouse)
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Pred. No. 0
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              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                  adhesion receptor).
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NCBI_TaxID=10090

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MGD; MGI:1859637; Nphal.
GO; GO:0005515; F:protein binding; II
GO; GO:0007254; P:JNK cascade; IDA.
GO; GO:000165; P:MAPKKK cascade; IDJ.
InterPro; IPR003957; FN III-like.
InterPro; IPR003961; FN III.
InterPro; IPR003961; FN III.
InterPro; IPR00398; Ig-1ie.
InterPro; IPR003598; Ig-22.
Pfam; PF00041; fn; 1.
Pfam; PF00047; ig; 8.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
C011 adhesion; Transmembrane; Signal,
 the European Bioinformatics Institute. There use by non-profit institutions as long a modified and this statement is not removed. I entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
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Shaw A.S., Holzman L.B., Mundel P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERACTION WITH CD2AP AND NPHS2. MEDLINE=21590460; PubMed=11733557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ∄.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21590051; PubMed=11733379;
Shih N.Y., Li J., Cotran R., Mundel P.,
"CD2Ap localizes to the slit diaphragm
novel C-terminal domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nephrin localizes cell.";
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MEDLINE=99436348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type I membrane protein (Potential) at podocyte slit diaphragm between podocyte foot process, TISSUB SPECIFICITY: Expressed in kidney glomeruli.
PTM: Phosphorylated on tyrosine residues (By similarity)
SIMILARITY: Belongs to the immunoglobulin superfamily.
SIMILARITY: Contains 8 immunoglobulin-like domains.
SIMILARITY: Contains 1 fibronectin type III domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Seems to play a role in the development or the kidney glomerular filtration barrier. May anchor slit diaphragm to the actin cytoskeleton. SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP domain.
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                                                                                                                                                                                                                                                                                                                                                                                        SMISS-PROT entry is copyright. It is produced through a collable of the Swiss Institute of Bioinformatics and the EMBL outst ruropean Bioinformatics Institute. There are no restrictions in the swiss Institute of Bioinformatics in an as its content is in
                                                                                                                                                                                                                                                                                                                                           AF168466; AAF03368.1; -
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IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 7.
IG-LIKE C2-TYPE 8.
FIBRONECTIN TYPE-III.
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CYTOPLASMIC (POTENTIAL).
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RESULT 93

LAC1 RAT STANDARD; PRT; 104

ID LAC1 RAT STANDARD; PRT; 104

AC P20756;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence upda

DT 10-OCT-2003 (Rel. 42, Last annotation up

DE Ig lambda-1 chain C region.

OS Rattus norvegicus (Rat).
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Eukaryota; Metazo Mammalia; Eutheri NCBI_TaxID=10116;

; Metazoa; Chordata; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat

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RESULT 94
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Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047; ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE
PROSITE; PS00200; IG_MC;
Immunoglobulin domain; Im
NON TER
1 1
DOMĀIN 6 99
DISULFID 27 85
DISULFID 103 103
SEQUENCE 104 AA; 11565
                                                                                                                                                                                                                                                                                                                                        Q05695;
Q01-FEB-1994 (Rel. 28, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Neural cell adhesion molecule L1 precursor (N-CAM L1)
L1CAM OR CAML1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Steen M.L., Hellman L., Petterson "The immunoglobulin lambda locus in genes and a single V lambda gene.", Gene 55:75-84(1987).
                                                                                                           Miura M., Kobayashi M., Asou H., Uyemura K.; "Molecular cloning of cDNA encoding the rat neural cell adhesion molecule Ll. Two Ll isoforms in the cytoplasmic region are produc by differential splicing "; FEBS Lett. 289:91
                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND MEDLINE=91372414; PubMed=1894011;
                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAML_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M22520; AAA41419.1; ALT_INIT.
HSSP; P01842; 7FAB
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MEDLINE=87305594; PubMed=3114047;
adhesion, neurite fasciculation, outgr
to axonin on neurons.
SUBCELLULAR LOCATION: Type I membrane
ALTERNATIVE PRODUCTS:
                                                                            FUNCTION: Cell adhesion molecule with development of the nervous system. Inv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50835; IG_LIKE; 1. PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||: | | | || || :: :| |: | || : : | |:::| | :: | | | : : 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPR-EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP-ENNYKTTPPVLD 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain; Immunoglobulin C
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 146; DB 1;
Pred. No. 0.0045;
9; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (WITH HEAVY CHAIN)
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                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                      outgrowth
                                                                            Involved in neuron-neuron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region.
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                   protein
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                                                        of neurites,
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InterPro; IPR003961; FN
InterPro; IPR007110; Ig
InterPro; IPR005598; Ig
InterPro; IPR005598; Ig
Pfam; PF00041; fn3; 4.
Pfam; PF00047; fg; 6.
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SMART; SM00408; IGC2; 5.

PROSITE; PS50835; IG LIKE; 6.

Neurogenesis; Cell adhesion; Developmental protein;

Transmembrane; Repeat; Immunoglobulin domain; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing. signal 1 19
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PIR; S36126; S36126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                CARBOHYD
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                  CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=2; Synonyms=Llcs;
IsoId=Q05695-2; Sequence=VSP 002592;
TISSUE SPECIFICITY; Isoform 2 Is predominantly found in the while isoform 1 is found in the peripheral nervous system. SIMILARITY: Belongs to the immunoglobulin superfamily. L1/neurofascin/NgCAM family.
L1/neurofascin/NgCAM family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type domains.
SIMILARITY: Contains 5 fibronectin type III domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative
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                                                                                                                                                                                                                                                                                                                                  517
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553
   CAA41860.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence=VSP 002592;
Y: Isoform 2 is predominantly found in the brain, s found in the peripheral nervous system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     splicing; Named isoforms=2;
                                                                                                                                                                                                                          IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 6.
FIBRONECTIN TYPE-III 1
FIBRONECTIN TYPE-III 3
FIBRONECTIN TYPE-III 3
GELL ATTACHMENT SITE (
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NEURAL CELL ADHESION MOLECULE
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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   (GLCNAC.
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P20763;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
13 lambda chain C region.
14 gallus (Chicken).
15 Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
16 Eukaryota, Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most proposed in the statement as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  EMBL; X04768; CAA28461.1; -. PIR; B26167; B26167. HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                          MEDLINE=87218480; PubMed=3107981;
Parvari R., Ziv E., Lentner F., Tel-Or S., Burstein Y., Schechter I.;
"Analyses of chicken immunoglobulin light chain cDNA clones indicate
a few germline V lambda genes and allotypes of the C lambda locus.";
EMBO J. 6:97-102(1987).
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                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 1 immunoglobulin-like domain.
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Best Local
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InterPro; IPR003597; Ig-c1.
InterPro; IPR003597; Ig-mHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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21-JUL-1986
21-JUL-1986
10-OCT-2003
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DISULFID
VARIANT
                                                                                                                                                                                                                                                                                                                                                           "The primary structure of a rat kappa Bence Jones protein: phylogenetic relationships of V- and C-region genes.";
J. Immunol. 115:59-62(1975).
SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sheppard H.W., Gutman G.A.;
"Allelic forms of rat kappa chain genes: evidence selection at the level of nucleotide sequence.";
Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Starace V., Querinjean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE (BENCE-JONES PROTEIN S211).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Louvain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
Ig kappa chain C region, B allele.
Rattus norvegicus (Rat).
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SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                     PIR; A93901; K1RTB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=75212238; PubMed=807630;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                      HSSP; P01842; 2MCG
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INTERCHAIN (WITH A HEAVY D -> N (IN REF. 2). N -> K (IN REF. 2). MISSING (IN REF. 2).
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A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
B Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Dutbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
A Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D.A., Heimann T.J., Wei M.-H., Ibegwam C.,
A Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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01-APR-1990 (Rel. 14, Created)
16-OCT-2001 (Rel. 40, Last sequence up
10-OCT-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Oregon-R;
MEDLINE=89028670; PubMed=3141062;
Seeger M.A., Haffley L., Kaufman T.C.;
"Characterization of amalgam: a member of the immunoglobulin superfamily from Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker S.E.,
Palazzolo M.J.;
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Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amalgam protein precursor.

AMA OR BG:DS00276.6 OR CG2198.
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RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Aliu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Aliu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Ala Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Ala Mentello K.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L., Ala Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L., Nelson D.R., Nelson D.L., Nelson D.R., Palson D.L., Nelson D.R., Palson D.L., Nelson D.R., Palson D.A., Nelson M.R., Palson D.M., Pellard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ala Shue B.C., Siden Kiamos I., Simpson M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Ala Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Ala Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Ala Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ala Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ala Milliams S.M., Venter E., Sheng L., Sheng L., Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Sibbs R.A., Myers E.W., Rubin G.M., Venter E., Sheng L., When M., Sheng L., Sheng X.H., Sheng R.M., Wenter S., Sheng R.S., Sheng R.S., Myers E.W., Rubin G.M., Venter S., Zhu X., Smith H.O., Shibs R.A., Myers E.W., Rubin G.M., Venter S., Sheng R.S., Shith H.O., Shibs R.A., Myers E.W., Rubin G.M., Venter S., Sheng L., Whatter S., Sheng R.S., Myers E.W., Rubin G.M., Venter S., Sheng R.S., Shith H.O., Shibs R.A., Myers E.W., Robin G.M., Venter S., Shith H.O., Shith H
                  Query Match
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    Matches
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STRAIN=Berkeley; TISSUE=Embryo;

MEDLINE=22426066; PubMed=12537569;

MEDLINE=22426066; PubMed=12537569;

Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,

George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan

George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan

Rubin G.M., Celniker S.E.;

"A Drosophila full-length cDNA resource.";

"A Drosophila full-length cDNA resource.";

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
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                                                                               SEQUENCE
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SMART; SM00408; IGc2; 2.
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EMBL; AY051911; AAK
PIR; A31923; A31923
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                    Similarity
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  form of a
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MEDLINE=94117008; PubMed=7507076;
Chhilsky M.I., Allan-ara VCAMI ge
                                                                                                                        STRAIN=NIH Swiss, and Kumar A.G., Dai Y.X., Ballantyne C.M.,
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92181437; PubMéd=1371918;
MEDLINE=92181437; PubMéd=1371918;
Mession C., Moy P., Tizard R., Chisholm P., Willie Burkly L., Miyake K., Kincade P., Lobb R.;
"Cloning of murine and rat vascular cell adhesion "Cloning of murine and rat vascular cell adhesion blochem. Biophys. Res. Commun. 183:163-169(1992).
                                      STRAIN=FVB; TISSUE=Lung;
MEDLINE=93232042; PubMed=7682556;
Moy P., Lobb R., Tizard R., Olson
                                                                                                                                                                                          Cybulsky M.I., Allan-Motamed M., Collins "Structure of the murine VCAM1 gene."; Genomics 18:387-391(1993).
                                                                                                                                                                                                                                                                                        "Cloning and sequencing Gene 126:261-264 (1993).
                                                                                                                                                                                                                                                                                                                              TISSUE=Lymph node
MEDLINE=93246254;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FVB; TISSUI
MEDLINE=92181437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular cell adhesion protein 1 precursor (V-CAM VCAM1 OR VCAM-1.
Moy P., Lobb R., Tizard R., Olson D., "Cloning of an inflammation-specific Form of murine vascular cell adhesion J. Biol. Chem. 268:8835-8841(1993).
                                                                                 SEQUENCE FROM N.A. (ISOFORM
                                                                                                            Submitted (AUG-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                SEQUENCE OF 1-693 FROM N.A.
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(Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                               node;
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Kozak C
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entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Kumar A.G., Dai X.Y., Kozak C.A.,
Ballantyne C.M.;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6; TIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycosylphosphatidylinositol-anchored VCAM protein.";
Proc. Natl. Acad. Sci. U.S.A. 90:5919-5923(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terry R.W., Kwee L., Levine J.F., Labow "Cytokine induction of an alternatively adhesion molecule (VCAM) mRNA encoding a
                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Endothelial cells;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Murine VCAM-1.
                                                                                                                                                                                                                                                                                                     IsoId=P29533-2; Sequence=VSP_002581, VSP_002582; TISSUE SPECIFICITY: Expressed on inflamed vascular endothelium, well as on macrophage-like and dendritic cell types in both normal inflamed tissue.

PTM: The GPI-anchor is located on position 319 of isoform 2. SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                                         Name=2; Synonyms=Short;
IsoId=P29533-2; Seque
                                                                                                                                                                                                                                                                                                                                                                       Name=1; Synonyms=Long;
IsoId=P29533-1; Sequence=Displayed;
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                                                                                                                                                                                                                                           and this statement is not removed
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EMBL; L22349; U12878; U12879; U12874; U12874; U12871; U12881; U12881; U12881; U12881; L22301; L22355; AAA16921. AAA16921. AAA16921. AAB60661 AAB60662 AAA16920 AAA16920 CAA47989.1; AAA16921 AAA16921.1; AAA16921.1; AAA16921.1; AAA40545.1; AAB60659 AAA16920 AAB60663 JOINED.
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EMBL; U12873; 
EMBL; U12873; 
EMBL; U12877; 
EMBL; L08431; 
EMBL; L08431; 
EMBL; L12541; 
EMBL; U42327; 
EMBL; U42327; 
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DOMAIN
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PRINTS; PR01472; ICAMYCAM1.
PRINTS; PR01474; VCAM1.
SMART; SM004008; IGc2; 3.
PROSITE; PS50835; IG LIKE; 5.
Immunoglobulin domain; Glycoprotein; Cell adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:98926; VCaml.
GG; GO:0007155; F:cell adhesion; IDA.
InterPro; IPR003987; ICAM VCAM-1.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-c2.
InterPro; IPR003989; VCAM-1.
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PIR; JN0581; JN0581.
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 391
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 TLEKRTQV-
                                 KVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKP----KDTLMISRTPEVTCV
                                                                       VVLTCAAIGCDSPSFSWRTQTDSPLNGVVRNEGAKSTLVLSSVGFEDEHSYLCAVTCLQR
                                                                                                          LTLTLESPPGSSPSVQCRSPRGKNIQG-----GKTLSVSQLELQDSGTWTCTVLQNQK
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                                                                                                                                                                        QGNFPLIIKNLKIEDSDTYICE----VEDQKEEVQLLV-----FGLTANSDTHLLQGQS
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AAA80014.
AAA80015.
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IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
IG-LIKE C2-TYPE 6.
IG-LIKE C2-TYPE 7.
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Pred. No. 0.0
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Missing (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINCED (GLCNAC. . .) (POTENTIAL).
EKPFIVDISPESQVAAQVODISVLTCAAIGCDSESF ->
GRMKSQITNGHQLTVHLMFAKSFYFICYLCLYLAL (in
                                                                                                                                                                                                                                                                                                                                                                           /FTId=VSP_002582.
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3D2134C341E5E449
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                                                                                                                                                                                                                                                                                                                                    DB 1; Length
                                                                                                                                                                                                                                                                                                 154;
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                                                                                                                                                                                                                                                                                                 Indels 123;
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(POTENTIAL).
(POTENTIAL).
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RESULT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pimenta A.F., Zhukareva V., Barbe M.F., Reinosc Henzel W., Fischer I., Levitt P.;
"The limbic system-associated membrane protein member that mediates selective neuronal growth Neuron 15:287-297(1995)
Pfam; PF0047; 13; 3.
SMART; SM00408; IGc2; 2.
PROSITE; PS50835; IG LIKE; 3.
Immunoglobulin domain; Cell adhesion; Glycoprotein; GPI-anchor; Repeat; Signal; Lipoprotein.
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMP_RAT
Q62813;
                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                               EMBL; U31554; AAA86120.1; -.
                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Limbic system-associated membrane protein pre
                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAMP OR LAMP
                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: MEDIATES SELECTIVE NEURONAL GROWTH AND AXON TARGETING. CONTRIBUTES TO THE GUIDANCE OF DEVELOPING AXONS AND REMODELING OF MATURE CIRCUITS IN THE LIMBIC SYSTEM. ESSENTIAL FOR NORMAL GROWTHE HYPPOCAMPAL MOSSY FIBER PROJECTION.

SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. TISSUE SPECIFICITY: Expressed mostly by neurons comprising limbic associated cortical and subcortical regions that function in cognition, emotion, memory, and learning.

COGNITION, emotion, memory, and learning.

DEVELOPMENTAL STAGE: FIRST DETECTED AT E15-16, AT STAGE E20 IT IS DETECTED IN PRESUMPTIVE CORTEX, MEDIAL LIMBIC AREAS OF THE THALAMUS AND HYPOTHALAMUS. IN THE ADULT, IT IS FOUND IN PRESUMPTIVE CORTEX, AMYGDALA AND MEDIAL THALAMIC PROTECTED IN THE ADULT, AND MEDIAL THALAMIC PROTECTED IN THE ADULT.
                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                    family.
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Sciurognathi; Muridae;
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and axon
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Tait S., Collinson J.
Submitted (NOV-2001)
                                                                                                                                        P97685; P97684; Q91Z60;
15-MAR-2004 (Rel. 43, Created)
15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
TISSUE=Brain;
MEDLINE=97103184; PubMed=8947556;
MEDLINE=97103184; PubMed=8947556;
                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                               NFAS_RAT
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                 TISSUE-Brain
                            SEQUENCE OF 25-1240
                                                                      SEQUENCE FROM N.A.
                                                                                                                 Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                              SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA---KTKPREEQ
                                                                                                                                                                                                                                                                                                                                    SQVYLIVQVPPKISNISSDVTVNEGSNVTLVCMANGRPEPVITWRHLTPLGREFEGEEEY
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                                                                                                                                                                                                                                                                                                                                                                                                                           LLLVLQLALLPAA-----TQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                                                                                                            YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                 LSVSQLELQDSGTWTCTVLQ-----NOKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGP
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EMBL/GenBank/DDBJ
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Pred. No. 0.
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                           (ISOFORMS
                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
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                           AND 3),
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                           SUBUNIT
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Ratcliffe C.F., Westenbrock R.E., Curtis R., Catterall W.A.;
"Sodium channel betal and beta3 subunits associate with neurofascin through their extracellular immunoglobulin-like domain.";

J. Cell Biol. 154:427-434(2001).

-I- FUNCTION: Cell adhesion, ankyrin-binding protein which may be involved in neurite extension, axonal guidance, synaptogenesis, myelination and neuron-glial cell interactions. Isoforms 2/3 may be responsible for mediating and signaling axon-glial interaction
                                                                                                                                                                                                                                                                                                                                                                                                                               Event-Alternative splicing; Named isoforms=3;
Name=1; Synonyms=NF186, 186 kDa isoform;
ISoId=P97685-1; Sequence=Displayed;
Name=2; Synonyms=NF155, 155 kDa isoform;
ISOId=P97685-2; Sequence=VSP_050416, VSP_050417, VSP_050418,
ISOId=P97685-2; Sequence=VSP_050416, VSP_050417, VSP_08417, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tait S., Gunn-Moore F., Collinson J.M., Huang Pedraza L., Sherman D.L., Colman D.R., Brophy "An oligodendrocyte cell adhesion molecule at the paranodal axo-glial junction.";
J. Cell Biol. 150:657-666(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION OF ISOFORMS 1 AND 2/3, INDIRECT PHOSPHORYLATION, AND TISSUE SPECIFICITY. MEDLINE=20391985; PubMed=10931875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98220650; PubMed-9562181; Collinson J.M., Marshall D., Gillespie C.S., Brophy P.J.; "Transient expression of neurofascin by oligodendrocytes at of myelinogenesis: implications for mechanisms of axon-glial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ankyrin-binding FNIII domain-) a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           during the early stages of myelination.

SUBNNT: Probable constituent of a neurofascin/NRCAM/ankyrin G complex. Associates with the sodium channel beta-1 (SCN1B) and beta-3 (SCN3B) subunits. Associates to beta-1 subunit in developing axons as early as postanated day 5, during the period that nodes of Ranvier are forming. Isoform 2/3 is likely to interact with axonal proteins in close association with CNTMAP1. SUBCELIULAR LOCATION: Type I membrane protein. Isoform 1 colocalizes with ankyrin G at the nodes of Ranvier. Isoform 2/3 is a glial component of the paranodal axo-glial junction.

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                       precipitously.

PTM: Isoform 2/3 is phosphorylated at P12.

required for ankyrin binding.

SIMILARITY: Belongs to the immunoglobulin
                                                                                                                                                                                                                                      L1/neurofascin/NgCAM family.
SIMILARITY: Contains 6 immunoglobulin-like C2-type d
SIMILARITY: Contains 4 fibronectin type III domains.
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135:1355-1367(1996).
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Pred. No. 0.15;
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Search completed: August 3, 2004, 13:09:30 Job time: 13.0314 secs

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A;Note: this sequence has the GIm(3) marker R;Rutishauser, U.; Cunningham, B.A.; Bennet Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human A;Reference number: A90564; MUID:71064025; A;Contents: Eu
                                                                                                   A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human
A;Reference number: A90563; MUID:71064024;
A;Contents : myeloma protein Eu
A;Accession: B90563
                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
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A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the Glm(17) allotypic marker,
A;Note: Lys-330 is removed after translation
                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C;Accession: A93433; 336861; $\overline{3}3887; \overline{8}90564; \overline{8}91\overline{6}8; \overline{A91723; A02146}
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 192.
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
                                                                                                                                                                                                                      A; Title: Structure of human immunoglobulin A; Reference number: $33887; MUID:83001943; A; Accession: $33887
                                                                                                                                                                                                                                                            R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, Cell 29, 671-679, 1982
                                                                                                                                                                                                                                                                                                                             A; Reference number: $33904
A; Accession: $36861
                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
                                                                                                                                                                                            ;Molecule type: DNA
;Residues: 88-113;235-330
                                                                            ;Molecule type: protein
;Residues: 1-96,'R',98-135 <CUN>
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Bennett,
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                                                                                                                                                                    Gall, W.E.; Gottlieb,
              gammaG-immunoglobulin. VIII. Amino acid
PMID:5530842
                                                                                                                                gammaG-immunoglobulin.
pMID:5489771
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PMID:6811139
                                     97-Arg
, C.; Konigsberg, W.H.; Edelman, G.M.
                                                                                                                                                                                                                                                                       T.; Nakai,
                                                                                                                                                                                                                                              implications for
                                                                                                                                                                                                                                                                                                                                                                                           97-Lys, and the Glm(1) markers,
                                                                                                                                                                                                                                                                        S.; Honjo,
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Ig mu chain C regi
T-cell surface gly
Ig alpha-1 chain C
Ig alpha-2 chain C
Ig alpha-2 chain C
Ig alpha-2 chain C
Ig mu chain C regi
Ig gamma-2b chain C r
Ig alpha chain C r
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g mu chain precur
g alpha chain C r
g alpha-2 chain C
g heavy chain S
g heavy chain, s
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g heavy chain, s
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y alpha chain
y alpha chain
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F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83;144-204,250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109;112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;F;20-85/Domain; immunoglobulin homology <IM1;
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A;Reference number: A90565, MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
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A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
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A; Molecule type: protein
A; Residues: 1-96; R; 98-197; D', 199-238; E', 240; M', 242-266; D', 268-271; D', 273-330
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
Biochemistry 9, 3188-3196, 1970
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A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Rote: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met
R;Ponstingl, H.; Hilschmann, N.
R;Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
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Best Local :
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ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                       GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                     NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                                                                                                                                      SSVVTVPSSSLGTQTYICNV--NHKPSNTKVD----KKVEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSVQCRSPRGKNIQGG------KTLSVS-----QLELQDSG----
                                                                                      NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                           GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                                                                                                                                                                                                                             PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSL 65
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74.5%;
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Pred. No. 7.1e-66;
7; Mismatches 22;
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PMID: 4923144
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Ig gamma-1 chain C region - synthetic C. Species: synthetic A. Note: Homo sapiens (man) gene engineered and expre C. Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #C. Accession: S31866 R.Filpula, D. Submitted to the EMBL Data Library, February 1993 A. Description: Screeing method for protein-protein i A.Reference number: S31866 A. Accession: S31866
                                                                                                                                                                                               RESULT
S31866
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R;Khamlichi, A.A.
submitted to the EMBL Data Library,
A;Reference number: S72664
A;Accession: S72664
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(Species: Homo sapiens (man)
(C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Bur. J. Biochem. 229, 54-60, 1995
Bur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339; MUID:95262687; PMID:7744049
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A; Residues: 1-140, 'C', 142-374 < KH2>
A; Cross-references: EMBL: X81695
C; Superfamily: immunoglobulin C reg
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                                                                                                             s (man) gene engineered and expressed in Escherichia
#sequence_revision 17-Mar-1997 #text_change 19-May-2
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                                        protein-protein interactions
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A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region
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A; Residues: 1-234 <EHR>
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A;Title: Nucleotide sequence of chimpanzee A;Reference number: PT0207; MUID:91287716; A;Accession: PT0207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig gamma chain C region - chimpanzee C;Species: Pan troglodytes (chimpanzee) C;Date: 23-Nov-1991 #sequence_revision C;Accession: PT0207
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                                                                                                                                                                                                                                                                                                                                          ;Superfamily: immunoglobulin C region; immunoglobulin;Keywords: immunoglobulin
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Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                            Matches 221;
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                 367
      176
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                                                                                                                                                                                                            192 KVEFKIDIVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTC
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ESSGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                    KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
                                                                                                                            VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                     ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                           VVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                KVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEW
                                                                                                                                                                                              KVDKKV-----EPKSCDTTHTCPPCAAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
                                                                                                                                                                                                                                                            Conservative
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97.4%;
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••
                                                                                                                                                                                                                                                                         Score 1173.5;
Pred. No. 7.6
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                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                         <MM>
                                                                                                                                                                                                                                                                                                                                                                                                                      Fc and hinge
PMID:2062315
                                                                                                                                                                                                                                                                           .6e-63;
                                                                                                                                                                                                                                                                                         DB 2;
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Ig gamma-3 chain C region (allotype G3m (Species: Homo sapiens (man) C;Date: 28-Dec-1987 #sequence_revision C;Accession: A23511 R;Huck, S.; Fort, P.; Crawford, D.H.; I

D.H.; Lefranc,

м. Р.,

Lefranc,

G3m(b)) -

human

28-Dec-1987

#text_change

23-Jul-1999

RESULT A23511

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R;Huck, S.; Lefranc, G.; Lefranc, M.P. Immunogenetics 30, 250-257, 1989 A;Title: A human immunoglobulin IGHG3 A;Reference number: A60764; MUID:90007. A;Accession: A60764
                                                                                                                                                                                                                                                                 Ig gamma-3 chain C region, form LAT - human C;Species: Homo sapiens (man) C;Decies: Homo sapiens (man) C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999 C;Accession: A60764 R;Huck, S.; Lefranc, G.; Lefranc, M.P.
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A; Residues: 1-377 < HUC>
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A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 16
C;Superfamily: immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-377 < HUC>
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A; Accession: A23511
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A;Title: Sequence of a human immunoglobulin
                                                                                                                                                                                   A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:X03604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: GDB:IGHG3
                                                                                                                  Superfamily: immunoglobulin C region; immunoglobulin; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-85/Domain: immunoglobulin homology <IMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keywords: immunoglobulin
                                                Local
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                                al Similarity
239; Conserv
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 TKGPSKLNDRADSRRS--
                                                                                                                                                                                                                                                                                                                                                                                                                      NYNTTPPMLDSDGSFFLYSKLTVDKSRWQQGNIFSCSVMHEALHNRFTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESSGQPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKGPSKLNDRADSRRS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELK----TPLGDTTHTCPRCPEP
                                                                                                immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.8%; Score 1157; DB 2; 57.3%; Pred. No. 1.3e-61;
                                                42.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n immunoglobulin gamma 3 heavy chain constant region MUID:86148507; PMID:3081877
                                                                                                                                                                                                                    ulin IGHG3 allele (Gmb0, b1, MUID:90007613; PMID:2571587
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                                              Score 1155;
Pred. No. 1.
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                                  Mismatches
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                                                .7e-61;
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                                                               Length 377;
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 ---NFPLIKNLKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSCDTPP---PCPRCPEPK-------SCDTPP-----SCDTPP-----
                                                                                                                                                                                                                                                                                                                                                                              PCP-APEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
NYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNRFTQKSLSLSPG
                             NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                       APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN 374
                                                                                                                                                                                                                                                                                     DPEVKFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVELK----TPLGDTTHTCPRCPEP 117
                                                                                                                                                                                                                                DPEVQFKWYVDGVEVHNAKTKPREEQYNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
                                                                                                             APIEKTISKTKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESSGOPEN
                                                                                                                                                                                                                                                                                                                                             PCPRCPEPKSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
  376
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Ig gamma-3 heavy chain disease proteins -

A; Contents: heavy chain disease A; Accession: A90442

A; Molecule type: protein
A; Residues: 1-289 < FRA>
A; Residues: 1-289 < FRA>
A; Residues: 1-289 < FRA>
A; Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain A; Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co
A; Note: the sequence of residues 42-76 was taken from the reference that follows
A; Nichaelsen, T.E.; Frangione, B.; Franklin, E.C.
J. Biol. Chem. 252, 883-889, 1977
J. Biol. Chem. 252, 883-889, 1977
A; Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication
A; Reference number: A92219; MUID:77118561; PMID:402363
A; Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W
A; Accession: A92219

A; Molecule type: protein A; Residues: 12-97 < MIC> A; Note: the hinge region in gamma-3 chains is about four times 86 long as Ħ gamma

A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C. Biochem. Biophys. Res. Commun. 71, 91, 1976
A;Title: The amino acid sequence of "heavy chain disease" protein A;Reference number: A90198; MUID:77021516; PMID:823945
A;Contents: heavy chain disease protein Zuc, partial sequence corr

corresponding

ö

residues

ZUC.

Structure

69,

72

form

A; Accession: A90198

A;Molecule type: protein
A;Residues: 59-125, 'EB',128-226,228-289 <WOL>
A;Residues: 59-125, 'EB',128-226,228-289 <WOL>
A;Rote: this protein lacks most of the V region, all of the R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982
A;Title: gamma heavy chain disease in man: cDNA sequence sup A;Reference number: A93915; MUID:88247835; PMID:6808505
A;Concents: heavy chain disease protein Omm B.; Œ 1 region,
Franklin, and part of , E.C.; Hood, gene

A;Accession: A93915 A;Molecule type: mRNA A;Residues: 12-70;72-114;116-125,'E',127-133,'L',135-136,'E',138,'Y',140-154,'D',156-157 A;Note: a carboxyl-terminal Lys is removed posttranslationally

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A;Title: The primary structure of a human IgG2 heavy chain: gend A;Reference number: A92809; MUID:81007873; PMID:6774012
A;Contents: myeloma protein Til
A;Accession: A92809
A;Molecule type: protein
A;Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WANNAMARCE: Trp-156 is at or near the complement-binding site R;Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain const A;Reference number: A90752; MUID:80001357; PMID:113060
A;Contents: myeloma protein Zie
A;Accession: A90752
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A;Residues: 1-326 <ELL>
A;Cross-references: GB:V00554; GB:J00230; NID:g32759; PIDN:CAB58438.1;
A;Note: Lys-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig gamma-2 chain C region - human (75Decides: Homo sapiens (man) (75Decides: A02148) (75Decides: A0316; A03132; A02148) (75Decides: A0316; A03132; A02148) (75Decides: A0316; A03132; A03148) (75Decides: A0316; A03148) (75Decides: A031488) (75Decides: A031488) (75Decides: A031488) (75Decides: A031488) (
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A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin c region; immunoglobulin; pyroglutamic acid C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid F;203-270/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gin) #status experimental
                                                                                                          A; Note: this sequence has since been revise R; Hoffmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A; Title: A note on the amino acid sequence A; Reference number: A93132; MUID: 80114419;
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A;Gene: GDB:IGHG3
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Best Local S
Matches 209
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protein
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                                                                                                                                                                                                                                                            60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q' been revised
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Pred. No. 2.
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PMID:118920
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A;Reference number: A90933
A;Accession: A90933
A;Molecule type: DNA
A;Residues: 1-327 <ELL>
A;Note: the sequence was derights, J.R.L.; Buttery, S
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A;A;Map position: 1492.33-14922.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kage) position: An immunoglobulin home cases, such as IgA and IgM, the subunits associate into learn disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into learn disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into learn cystomerical immunoglobulin cases, such as IgA and IgM, the subunits associate into learn cystomerical immunoglobulin cases, such as IgA and IgM, the subunits associate into learn cystomerical immunoglobulin homology <IM1>
F;20-85;Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;147Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;27-83,140-200,246-304/Disulfide bonds: interchain (to hain) #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to hain) #status experimental
                                                                                                                                                                        R;Ellison, J.; Buxbaum,
DNA 1, 11-18, 1981
                                                                                                                                                                                                                   Ig gamma-4 chain C region - human C;Species: Homo sapiens (man) C;Date: 02-Apr-1982 #Bequence revision C;Accession: A90933; A90249; A02150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Milstein, C.; Frangione, B.
Blochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bonds
A;Contents: number; Pink, JR.L.
Nature 221, 145-148, 1969
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R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, Marc
A;Reference number: A94591
A;Contents: annotation; Zie,
                                                                                                                           A; Title: Nucleotide sequence of a human immunoglobulin A; Reference number: A90933; MUID:83157104; PMID:6299662
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVKGFYPSDIAVEMESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGNVFSCSV
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82.6%;
  determined from S.H.; De Vries,
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Pred. No. 4e-6
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     the germline gene G.M.; Milstein, C
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PMID:5782707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4e-60;
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in having
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                                                                                                                                                  C-gamma4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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60-Ala and
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N;Alternate names: T-cell surface antigen T4/Leu 3
C;Species: Homo sapiens (man)
C;Becies: Homo sapiens (man)
C;Accession: A90872; A32722; A34194; A53287; I54176; I54297; A02109; A30039
C;Accession: A90872; A32722; A34194; A53287; I54176; I54297; A02109; A30039
R;Maddon, P.J.; Littman, D.R.; Godfrey, M.; Maddon, D.E.; Chess, L.; Axel, R.
Cell 42, 93-104, 1985
A;Title: The isolation and nucleotide sequence of a cDNA encoding the T cell A;Reference number: A90872; MUID:85254948; PMID:2990730
A;Accession: A90872
                                                                                   Cell
                                                                                                                      Cell 55, 541, 1988
A;Title: Corrected CD4 sequence.
A;Reference number: A90907; MUID:89028665; PMID:3263213
A;Contents: annotation; revision to residue 26
R;Camerini, D.; Seed, B.
                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-25,'N',27-458 <MAD>
A;Experimental source: clone pT4B
R;Littman, D.R.; Maddon, P.J.; Axel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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F;240-307/Domain: immunoglobulin homology <IM3>
F;240-307/Domain: immunoglobulin homology <IM3>
F;14/Disulfide binds: interchain (to light Chain) #status experimental F;27-83,141-201.247-305/Disulfide bonds: #status predicted F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:119340; OMIM:147130
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 111/1; 221/1
C;Complex: An immunoglobulin heterotetramer
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A; Title: A CD4 domain important for HIV-mediated syncytium formation A; Reference number: A32722; MUID:90182664; PMID:2107024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell surface glycoprotein CD4 precursor [validated] - N;Alternate names: T-cell surface antigen T4/Leu 3
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A; Residues: 1-30;81-326 < PIN>
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A;Accession: A90249
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83.7%;
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; Pred. No. 1:9e-59; 
11; Mismatches 15
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

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A;Molecule type: mRNA
A;Residues: 26-426, 428-458 <CAM>
R;Carr, S.A.; Henling, M.E.; Folena-Wasserman, G.; Sweet,
R;Carr, C.A.; Henling, M.E.; Folena-Wasserman, G.; Sweet,
J. Biol. Chem. 264, 21286-21295, 1989
A;Title: Protein and carbohydrate structural analysis of
A;Reference number: A34194; MUID:90078232; PMID:2592374
A;Contents: disulfide bonds; carbohydrate-binding sites
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A;Title: Humans with OKT4-epitope deficiency have a single A;Reference number: I54297; MUID:91216786; PMID:1708753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 14, 590-597, 1992
A;Title: A human dimorphism resulting from loss of an Alu.
A;Reference number: I54176; MUID:93052387; PMID:1330888
A;Accession: I54176
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A;Gene: GDB:CD4
A;Cross-references: GDB:119767; OMIM:186940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-264,'W',266-458 <RE2>
A;Cross-references: GB:M35160; NID:g179143; PIDN:AAA16069.1; PID:g179144
C;Comment: Macrophage tropic strains of HIV-1 bind to a complex of chemokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 12pter-12p12
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A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: sequence extracted f
R; Edwards, M.C.; Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 250-264,'W',266-280 <LED>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: A53287
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A;Status: nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology; Keywords: AIDS; duplication; glycoprotein; T-cell; transmembrane protein; I-25/Domain: signal sequence #status predicted <SIG>
3.26-458/Product: T-cell surface glycoprotein CD4 *status experimental <MAT>
3.26-458/Product: T-cell surface glycoprotein CD4 *status experimental <MAT>
3.136-186/Domain: immunoglobulin homology <IM1>
3.136-186/Domain: immunoglobulin homology *status atypical <IM2>
3.216-299/Domain: immunoglobulin homology <IM3>
3.21-372/Domain: immunoglobulin homology <IM4>
3.321-372/Domain: transmembrane #status predicted <IMM>
3.421-458/Domain: transmembrane #status predicted <IMT>
3.41-109,155-184,328-370/Disulfide bonds: #status experimental
3.41-109,155-184,328-370/Disulfide bonds: #status experimental
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\;Residues: 26-394 <CRR>
\;Residues: 27-394 < CRR
\;Residues: 27-3
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Best Local Similarity
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLIVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                       MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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99.5%;
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Pred. No. 1.5e-5
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.5e-53;
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A; Accession: A02155
A; Accession: A02156
A; Molecule type: DNA
A; Residues: 1-398 <WEL>
A; Residues: 1398 <WEL>
A; Residues: 1298 <WEL>
A; Roserrecas: GB:J00451; NID:g194392; PIDN:AAB59655.1; PID:g194433
A; Note: the sequence was determined from the germline gene
A; Note: the sequence was determined from the germline gene
A; Note: the structure of the mouse immunoglobulin in gamma-3 membrane gene segment.
A; Reference number: A02155; MUID:84041483; PMID:6314258
A; A; Ccession: A02155
A; Accession: A02155
A; Accession: A02155
A; Mote: the sequence was determined from the germline gene
C; Genetics: 328-332, 'G', 334-341, 'Q', 343-387, 'F', 389-398 <KOM>
A; Residues: 328-332, 'G', 334-341, 'Q', 343-387, 'F', 389-398 <KOM>
A; Cross-references: GB:K00688
A; Note: the sequence was determined from the germline gene
C; Genetics: 97/1; 113/1; 223/1; 328/1; 371/3
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaphain disputfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F: 7:71-112/Recion: hinde
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C/Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text
C/Accession: A02156, A02155
R/Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Mar
EMBO J. 3, 2041-2146, 1984
A/Title: Structure analysis of the murine IgG3 constant
A/Reference number: A02156; MUID:85027161; PMID:6092053
G1MSM
Ig gam
C;Spec
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F;136-205/Domain: immunoglobulin homology <IM2>
F;242-309/Domain: immunoglobulin homology <IM3>
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g gamma-1
;Species:
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Best Local
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Date: 13-Aug-1986 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
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chain C region, memb
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                                                                                                                                                                                                                                                               REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDT
                                                                                                                                                                                                                                                                                                                 RDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                                                                                                                                                        QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP
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                                                                                                                                                         DSWLQGE1FTCSVVHEALHNHHTQKNLSRSPELELNETCAEAQDGELDGLWTT
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                           mouse
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A;Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunog F;131-200/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 17-Dec-1982 #sequence_revision 31-Mar-1991 #text_ch C;Accession: B02159; A02160; B02158 R;Honjo, T; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Cell 18, 559-568, 1979 A;Title: Cloning and complete nucleotide sequence of mouse A;Reference number: A02159; MUID:80045036; PMID:115593
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A; Residues: 323-393 < TYL>
R; Rogers, J.; Choi, E.; Souza,
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A;Molecule type: DNA
A;Residues: 1-393 <HON>
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A; Residues: 323-366 < ROG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
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Best Local
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323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 LLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQ--NQ
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                                                                      GLQLDETCAEAQDGELDGLWTT 452
                                                                                                                                                 QPAENYKNTQPIMNTNGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSP
                                                                                                                                                                                                                QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
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Pred. No. 2.9e-48;
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Ig heavy chain precursor (B/MT.4A.17.H5.A5) . N;Alternate names: Ig gamma-1 chain C region C;Species: Bos primigenius taurus (cattle)

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C;Date: 06-Jan-
C;Accession: S2
R;Sanders, P.G.
Ig gamma-2a chain C region, membrane-bound form -
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1984 #sequence_revision 31-Mar-1991
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A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Superfamily: immunoglobulin C region; immunoglobulin; membrane protein
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (ABN) (covalent) #status predicted
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A; Residues: 1-470 <SAN;
A; Cross-references: EMBL: X62916; NID: 9439; P
A; Cymons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A; Title: Structure of bovine immunoglobulin
A; Reference number: S06610; MUID: 90097956; P
A; A; A; Crossion: S06610
                                                              G2MSAM
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A;Residues: 142-470 <SYM>
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AHPASSTKVDKAVD----PTCKPSPCD---CCPPPELPGGPSVFIFPPKPKDTLTISGTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQ--NQKKYEFKIDIVPCPAPEPKSCDKTHTC--PELLGGPSVFLFPPKPKDTLMISRTP 242
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#sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
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Pred. No. 3.7e-47;
2; Mismatches 136;
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Immunol. 153,

I.; Sun, J.; Butler, 53, 3565-3573, 1994

cic pig) 21-Feb-1997

#text_change

21-Jan-2000

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Ig gamma 2a chain constant region - pig (fc;Species: Sus scrofa domestica (domestic C;Date: 21-Feb-1997 #sequence_revision 21-C;Accession: I47159
R;Kacskovics, I.; Sun, J.; Butler, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 373-399 <RES>
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C;Comment: The sequence of residues 1-328 was assumed to be identical with the correspon C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma hat it contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: the sequence was determined from the germline gene R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T. Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: B32657
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A,Title: Nucleotide sequences of gene segments encoding A,Reference number: A02154; MUID:82222190; PMID:6283537
A,Moleonia ****
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associal
C;Superfamily; immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Immunol. 26, 819-826, 1989
A;Title: Sequence and polyadenylation site determination of the murine immunoglobulin A;Reference number: I57809; MUID:90097953; PMID:2513486
A;Accession: I57809
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A;Cross-references: GB:J00471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 346
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                                                                                                                                                                                                                                               SYSCSVVHEGLHNHHTTKSFSRTPGLDLDDVCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                       QVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKK 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---PCKC----PAPNLLGGPSVF
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A;Title: Five putative subclasses of swine IgG identified A;Reference number: I47158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
A;Crqss-references: EMBL:U03779; NID:g433123; PIDN:AAA5221
C;Genetics: A;Grqs: immunoglobulin C region; immunoglobulin homology <IMM's
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
A; Residues: 1-47, 'E', 49-71, 'PV', 72-128 < PRA>
A; Residues: 1.47, 'E', 49-71, 'PV', 72-128 < PRA>
R; Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
R; Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
A; Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain
A; Reference number: A33928
A; Recession: A93928
A; MUID: 83299917; PMID: 6193512
A; Accession: A93928
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 < MAR>
A; Residues: 88-103, 'M', 105-143, 'E', 145-184, 'A', 186, 'E', 188-266 < MAR>
A; Cross-references: GB.M16426; NID: g165111; PIDN: AA311289.1; PID: g165112
A; Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
Biochem. J. 116, 249-259, 1970
                                                                                                                                                                                                                                                                                                    A;Note: this sequence has the d12 allotypic R;Pratt, D.M.; Mole, L.E. Biochem. J. 151, 337-349, 1975
A;Title: Sequence studies on the constant 1 A;Reference number: A90290; MUID:76135469; A;Accession: A90290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig gamma chain C region - rabbit (;Species: Oryctolagus cuniculus (domestic rabbit) C;Species: Oryctolagus cuniculus revision 15-Nov-1984 #t C;Date: 24-Apr-1984 #sequence revision 15-Nov-1984 #t C;Accession: A91749; A90290; A93928; A90245; A94416; R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G. Immunogenetics 18, 387-397, 1983
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A; Residues: 1-323 <BER>
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Matches 182
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Pred. No. 1.7e
38; Mismatches
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Ig gamma 4 chain constant region - pig (fragment) C;Species: Sus scrofa domestica (domestic pig) C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 C;Accession: I47162 R;Kacskovics, I.; Sun, J.; Butler, J.E. J. Immunol. 153, 3565-3573, 1994 J. Immunol. 153, 3565-3573, 1994 A;Title: Five putative subclasses of swine IgG ider A;Reference number: I47158; MUID:95015845; PMID:793
                                                                                                                                                                                               A;Gene: IgG4
C;Superfamily: i
F;82-151/Domain:
                                                                                                                                                                                                                                                                                                                                                   A;Accession: I47162
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-277 <KAC>
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A; Residues: 129-131; 155-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q', A; Residues: 129-131; 155-172, 'D', 174-184, 'A', 185-Ala
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C; Complex: An immunoglobulin heterotetramer subunit consist
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C;Genetics:
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A;Accession: A94416
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                                                                         Query Match
Best Local S
Matches 172
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            TLSVSQLELQDSGTWTCTVLQNQKKVEFKID-----IVPCPAPEPKSCDKTHTCPELL
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homology <IMM>
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Pred. No. 2.2e
34; Mismatches
                                                                      Score 898; DB
Pred. No. 2.1e
33; Mismatches
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TVPASSL---SSKSYTCNV--NHPATTTKVDKRVGTKTKPPCP-

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RESULT 19
G2GP
            Ig gamma-2 chain C region - guinea pig C;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence revision 07-May-1981 #sequence revision 07-May-1981 #set che C;Accession: A94553; A90352; A90359; A90384; A90385; A02151 C;Accession, T.M. submitted to the Atlas, April 1975 A;Reference number: A94553
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A;Gene: IgG2b
C;Superfamily: immunoglobulin C region; immunoglobulin
F:133-202/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-328 <KAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Five putative subclasses of swine A;Reference number: I47158; MUID:95015845; A;Accession: I47160
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
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R;Kacskovics, I.; Sun, J.; Butler, J.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 TLSVSQLELQDSGTWTCTVLQNQKKVEFKID-----IVPCPAPEPKSCDKTHTCPELL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      G-GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
                                                                                                                                                                                                                                                                                                                                                                                                                    SPGPSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEE
                                                                                                                                                                                                                                DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                 QFNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPGPSAFIFPPKPKDTLMISRTPKVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEE
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                                                                                                                                                                                                            DKASWQGGGIFQCAVMHEALHNHYTQKSISKTPG
                                                                                                                                                                                                                                                                              AEELSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSV
                                                                                                                                                                                                                                                                                                            RDELTKNOVSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLDSDGSFFLYSKLTV 397
                                                                                                                                                                                                                                                                                                                                                                                   QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVPASSL---SSKSYTCNV--NHPATTTKVDKRVGTKTKPPCP-----ICPACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DKASWQRGDTFQCAVMHEALHNHYTQKSIFKTPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QPNSTYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: U03780; NID: g433125; PIDN: AAA52218.1; PID: g433126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 898; DB 2;
Pred. No. 2.6e-46;
                                                                               07-May-1981 #text_change 16-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                              397
                                                                                                   339
                                                                                                                                      175
295
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                                                                                                                                                                                                           115
                                                                                                                                                                                                                                           219
                                                                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                              58
VDKSAWDQGTVYTCSVMHEALHNHVTQKAISRSPG
              VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                 SRDELSKSKVSVTCLIINFFPADIHVEWASNRVPVSEKEYKNTPPIEDADGSYFLYSKLT
                                                                                                                                                                                                                                                                                                                                                  Conservative
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A;Molecule type: protein
A;Residues: 227-311 cTR2>
R;Oliveira, B.; Lamm, M.E.
Biochemistry 10, 26-31, 1971
A;Reference number: A90354; MUID:71058474; PMID:4922544
A;Contents: annotation; disulfide bonds
A;Note: Cys-16 is involved in a heavy-light chain bond
A;Note: Cys-16; Cys-107, and Cys-10 form inter-heavy chain bonds
C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C;Comment: This chain was isolated from pooled serum of strain and inbred guinea pigs.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin cregion; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;21-81/Domain: immunoglobulin homology
C;Keywords: immunoglobulin homology c;TM2
E: 135-204/Domain: immunoglobulin homology c;TM2
E: 135-204/Domain: immunoglobulin homology c;TM2
E: 135-204/Domain: immunoglobulin homology c;TM2
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A;Residues: 134-226 <TRA>
R;Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A;Title: Primary structure of the C-H3 homology region 1
A;Reference number: A90385; MUID:75036073; PMID:4609467
A;Accession: A90385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;135-204/Domain: immunoglobulin homology <1M2>
F;241-310/Domain: immunoglobulin homology <1M3>
F;248-79/Disulfide bonds: #status experimental
F;142-202/Disulfide bonds: #status experimental
F;178/Binding site: carbohydrate (Asn) (covalent)
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A;Residues: 69-133;312-329 <TUR>
R;Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A;Title: Primary structure of the C-H2 homology region 1
A;Reference number: A30384; MUID:75036072; PMID:4429665
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A; Residues: 4-68 <BIR>
R; Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A; Title: Structure of heavy chain from strain 13 guinea
A; Reference number: A90359; MUID:71058486; PMID:5538616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Birshtein, B.K.; Hussain, Q.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A;Title: Structure of heavy chain from strain 13 guinea
A;Reference number: A90352; MUID:71058471; PMID:5538606
A;Accession: A90352
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A; Residues: 1-3
R; Birshtein, B.K
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                                                                                                                                                                                                                                    NIGGPSVEIFPPKPKDTIMISLTPRVTCVVVDVSQDEPEVQFTWFVDNKPVGNAETKPRV 174
                                                                                                                                                                                                                                                                                    LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 278
SRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLDSDGSFFLYSKLT 396
                                                                                                  EQYNTTFRVESVLPIQHQDWLRGKEFKCKVYNKALPAPIEKTISKTKGAPRMPDVYTLPP
                                                                                                                                               EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 338
                                                                                                                                                                                                                                                                                                                                                                  LOSGLYSLTSMVTVPSSQKATCNVAHPASSTKVDKTVEPIRTPZPBPCTCPK---CPPPE
                                                                                                                                                                                                                                                                                                                                                                                                                               IQGGKTLSVSQLELQDSGTWTCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTC--PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.1%; Score 894.5; DB 1 62.5%; Pred. No. 4.2e-46;
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Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A;Title: Nucleotide sequences of gene segments encoding A;Reference number: A02154; MUID:82222190; PMID:6283537
A;Moleonia -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;KBCSKOVICS, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine
A;Reference number: I47158; MUID:95015845;
A;Accession: I47158
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G2MSBM
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C;Superf
A;Title: Gene segments encoding transmembrane carboxyl termini A;Reference number: A02158; MUID:82115295; PMID:6799207 A;Accession: A02158
A;Molecule type: DNA A;Residues: 335-378 <ROS>
A;Note: the translation of the first exon of the membrane-bound
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C;Genetics:
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A; Residues: 1-328 < KAC>
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                                                                                                            A;Cross-references: GB:J00462
R;Rogers, J.; Choi, E.; Souza, L.;
Cell 26, 19-27, 1981
                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 335-405 < YAM>
                                                                                                                                                                                                                                                                                                 Ig gamma-2b chain C region, membrane-bound form - mouse C;Species: Mus musculus (house mouse) C;Date: 17-Dec-1982 #sequence revision 31-Mar-1991 #text_change C;Accession: C02154; A02158; B02157
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Best Local S
Matches 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSVLPIQHQDWLKGKEFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSRSK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ
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in: immunoglobulin homology <IMM>
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#веquence_revision 21-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: U03778; NID: g433121; PIDN: AAA52216.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.5%; Score 879.5; DB 2
55.2%; Pred. No. 3.3e-45;
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                                                                                                                                Carter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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 of the membrane-bound
                                                                                                                                c.,
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                                                                                                                                Word,
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                                                                                                                                M.; Eisenberg,
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C;Species: Fan Lryston.
C;Date: 30-Sep-1993 #sequence
C;Accession: B32722; A46534
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
Cell 60, 747-754, 1990
R;Pomsgaard, A.; Hirsch, V.M.; Johnson, P.R.
Eur. J. Immunol. 22, 2973-2981, 1992
A;Title: Cloning and sequences of primate CD4 molecules:
A;Reference number: A46534; MUID:93049640; PMID:1425921
A;Accession: A46534
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-335,'K' <YA2>
G;Comment: The sequence of residues 1-334 was assumed to be identical with the correspor C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The mathat it contains an alternative 3' end, encoded in separate exons, that is homologous with
                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-432 < CAM>
A; Cross-references: GB: M31135
                                                                                                                                                                                                                                            A;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722; MUID:90182664; PMID:2107024 A;Accession: B32722
                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;186/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Pan troglodytes (chimpanzee);Date: 30-Sep-1993 #text_change 16-Jul-1999;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                             chimpanzee
antigen T4/Leu
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A;Residues: 3-399 <FOM>
A;Note: sequence extracted from NCBI backbone (NCBIP:118332)
A;Note: sequence extracted from NCBI backbone (NCBIP:118332)
C;Comment: This protein is expressed on most thymocytes, on a subset of mature (Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication; glycoprotein; T-cell; transmembrane protein P;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F;1-371/Domain: extracellular #status predicted <EXT>
F;9-86/Domain: immunoglobulin homology <IM1>
F;111-161/Domain: immunoglobulin homology *IM3>
F;296-347/Domain: immunoglobulin homology <IM3>
F;296-347/Domain: transmembrane #status predicted <TMM>
F;396-432/Domain: intracellular #status predicted <TMM>
F;16-84,130-159,303-345/Disulfide bonds: #status predicted
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
C;Accession: 147161
C;Accession: 147161
R;Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol, 153, 3565-3573, 1994
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;133-202/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-328 < KAC>
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Best Local Similarity
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                                                                                                                                                                                                                                   191
                                                                                                                                                                                                                                                                                                                            137 QSLTLT-----LESPPGSSPSVQCRSPRG-KNIQGGKTLSVSQLELQDSGTWTCTVLQNQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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EFKCKVNNVDLPAPITRTISKAIGQSREPQVYTLPPPAEELSRSKVTVTCLVIGFYPPDI
                                       EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI 362
                                                                                                                                    EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 302
                                                                                                                                                                                     PATTTKVDKRVGTKTKPPCP------ICPGCEVAGPSVFIFPPKPKDTLMISQTP
                                                                                                                                                                                                                                 KKVEFKID-----IVPCPAPEPKSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTP 242
                                                                                                                                                                                                                                                                                  EPVTMTWNSGALTSGVHTFPSV--LQPSGLYSLSSMVTVPASSL---SSKSYTCNV--NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDQGNFTLIIKNLKIEDSDTYICEVGDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVEGLTANSDTHLLQGQSLTLTLESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQTKILGNQGSFLTKGPSKLNDRVDSRRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIV
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                          32.3%; Score 873; DB 2
57.6%; Pred. No. 8e-45;
rative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 875; DB 1;
Pred. No. 8.4e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from GB/EMBL/DDBC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IgG identified PMID:7930579
                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                             61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 328;
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A; Introns:
C; Complex:
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Peb-1998 #sequence_revision 13-Mar-1998 #text_change 21
C;Accession: PC4436
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; K
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap; hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu C;Keywords: immunoglobulin homology <IMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: B02156
R;Wels, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, EMBO J. 3, 2041-2046, 1984
A;Title: Structure analysis of the murine IgG3 constant region gene.
A;Reference number: A02156; MUID:85027161; PMID:6092053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig gamma-3 chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) C;Date: 17-Mar-1987 #sequence_revision 31-Mar-1991 C;Accession: B02156
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A; Residues: 1-329 <WEL>
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                                                                                                                                                                           PC4436
                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;136-205/Domain: immunoglobulin homology <IM2>F;242-309/Domain: immunoglobulin homology <IM3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: the sequence was determined from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B02156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;Genetics:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                       RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVSQLELQDSGTW-----TCTVLQNQKKVEFKIDI---VPCPAPEPKSCDKTHTCP--EL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                     REQMSKKKVSLTCLVTNFFSEAISVEWERNGELEQDYKNTPPILDSDGTYFLYSKLTVDT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QYNSTFRVVSALPIQHQDWMRGKEFKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGGPSVFIFPPKPKDALMISLTPKVTCVVVDVSEDDPDVHVSWFVDNKEVHTAWTQPREA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.7%; Score 857.5; DB 1 59.6%; Pred. No. 6.7e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #status predicted
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                                                                                                     21-Jan-2000
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A;Reference number: JC5810; MUID:98063277; A;Accession: PC4436 A;Molecule type: protein

H.; Kamachi, M.; Harada,

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13-1 against

porphyr

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RESULT 26
$31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis
C;Date: 13-Jan-1995 #sequence_revision
C;Accession: S31459
R;Patri, S; Nau, F
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                                                                                                                  Query Match
Best Local S
Matches 196
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Best Local S
Matches 188
                                                                                                                                                                                       Superfamily: immunoglobulin C region; immunoglobulin; Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Comment: This catalytic antibody has peroxidase oxidase activity. It is ;Superfamily: immunoglobulin C region; immunoglobulin homology ;251-320/Domain: immunoglobulin homology <IMM> ;27/Disulfide bonds: interchain (to 98) #status predicted ;99/Disulfide bonds: interchain (to 109) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   399
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                                                                                                                               n 31.6%;
Similarity 42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNS--GSLSSGVHTFPA---VLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIS-RDDSKSSVYLOMN-----RLREEDTATYYCCRTPWVYAMDCWGQGTSVIVSSAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGKKGDTVELTCTAS--QKKSIQFHW------KNSNQIKIL------GNQGSFLTKGPS
                              LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEE------VQLLVFGLTANSDTHL
                                                          TLSVTCTISGFSLNNYGVDWVRQAPGKALEWLGGSGYDEDIDYNPVLKSRLSITKDTSKS
                                                                                       TVELTCTAS---QKKSIQFHWKN----SNQIKILGNQG---SFLTKGP----SKLNDRADSRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCGC-KPCIC----TVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKTLSVSQLELQDSGTW-----TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QKEEVQLLVFGLTANSDTHLLQG-----QSLTLTLESPPGSSPSVQCRSPRGKNIQG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVRPGNSLKLSCLTSGFTFSNYRMHWLRQPPGKRLEWIAVITVKSDNYGAKYAESVRGRF
   ----QVSLTLSTVTTEDTAVYYCARVDYDSSHAFAYASYDFWGPGLLISVLSAST----
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYIC-----EVED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.6%; Score 854.5; DB 2;
41.5%; Pred. No. 1.4e-43;
tive 76; Mismatches 118;
                                                                                                                  ; Score 854.5; DB 2;
; Pred. No. 1.5e-43;
55; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        443
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                                                                                                                                                                                                                               LTLTLESPPGSSPSVQ-----CRSPRGKNIQGG------KTL-----
                                                                                                                                                                                                                                                                                                                     LVKPGASVKISCKASGYTFTDYY---INWVKQKPGQGLKWIGWIYPASGNTKYNENFKGK
REPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGS
                                                                                    KC----PAPNILGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVE
                                                                                                               SCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
                                                                                                                                           PAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRGPTIKPCP---PC
                                                                                                                                                                                                                                                                                         RSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQS
                              VHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSV
                                             VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                                        -SVSQLELQ-----DSGTW-----TCTVLQ--NQKKVEFKID-----IVPCPAPEPK 208
                                                                                                                                                                                                 TTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTF
                                                                                                                                                                                                                                                              ATLTVDTSSSTAYMQLSSLTSEDTAVYFC-----ARAMGATAT----LLDYWGQG
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428 SYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPG 471	b
388 SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431	У З
368 EPQVYVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGTTTSQLDADG 427	В
330 EPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG 387	У з
308 RTARTKPREEQFNSTFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAR 367	3
270 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 329	Y 2
251RCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEV 307	b 2
212 KTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 269	¥ 2
194 FPAILQSSGLYSLSSVVTVPASTSGAQTFICNVAHPASSTKVDKRVE-PGCPDP-CKHC- 250	b 1
174 LELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCD 211	y 1
145TPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVTVTWNSGALTSGVHT 193	ъ ъ
134 LQGQSLTLTLESPPGSSPSVQCRSPRGKNI	Y 1

A;Accession: \$37483
A;Status: preliminary
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1;
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM> Ig gamma-2a chain - mouse
(;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: \$37483
R;Ducancel, F.F.D. 30 LGKKGDTVELTCTASOKKSIQFHWKNSNQIKILGNOG-----SFLTKGPSKLNDRADSR Conservative 31.5%; Library, 56; Score 850.5; DB 2 Pred. No. 2.7e-43; 6; Mismatches 125 February 06-Jan-1995 #text_change 23-Jul-1999 125; 2 Indels Length PID: 9406253 85; Gaps 83

365

328

305 268 249

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C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 C;Accession: C30554 R;Foley, R.C.; Beh, K.J.
J. Immunol. 142. 70a-711
                                                   A; Molecule type: DNA
A; Residues: 1-333 <BRU>
A; Residues: 1-333 <BRU>
A; Residues: 1-334 <BRU>
Broc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986

Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A; Title: Immunoglobulin heavy chain locus of the rat: striking A; Reference number: A25941; MUID:86287397; PMID:3016742
A; Accession: B25941
                                                                                                                                                                              Gene 74, 473-482, 1988
A; Title: Evolution of the r:
A; Reference number: PS0017;
A; Accession: PS0018
A; Molecule type: DNA
A: Residues: 227-333
                                                                                                                                                                                                                                                                         C;Date: 07-Jun-1990 #sequence_revision
C;Accession: PS0018; B25941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Isolation and sequence of sheep Ig H and L chain cDNA. A;Reference number: A30554; MUID:89093962; PMID:2492052 A;Accession: C30554
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                                                                                                                                                                                                                                                        R;Brueggemann,
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                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain C region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Keywords: heterotetramer; immunoglobulin
;113-182/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                             y gamma-2b chain C region - rat
;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g heavy chain C region - sheep (fragment);
Species: Ovis orientalis aries, Ovis amm
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTTVPASTSGAQTFICNVAHPASSTKVDKRVE-PGCPDP-CKHC----RCPPPELPGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TFRVVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRTISRTKGQAREPQVYVLAPPQEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQFSWFVDNVEVRTARTKPREEQFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVSQLELQDSG--TWTCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTC--PELLGGP
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 <BR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.0%;
60.7%;
                                                                                                                                                                                                   rat immunoglobulin gamma heavy-chain 7; MUID:89232738; PMID:3149946
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Pred. No. 8
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                                                                                                                         S.; Waldmann,
                                                                                       homology to mouse
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Ig gamma-2a chain (mbb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision
C;Accession: S40295
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;20-82/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                      F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;22-96,144-199,261-321,367-4210 sludfide bonds: #status predicted F;122/Disulfide bonds: interchain (to light chain) #status predicted F;124,227,229/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                              F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic F;1-446/Product: Ig gamma-2a chain #status experimental <MAT> F;1-17/Domain: V-D-J region <VDJ> F;118-446/Domain: C region <CHR> F;118-214/Domain: C1 region <CHR> F;118-214/Domain: C1 region <CHI> F;215-230/Region: hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 a.
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-446 <KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S40295
A; Accession: S40295
                                                                                                                                                                                                                                                                 ;297/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STWPSQTVTCNVAHPASSTKVDKKVERRNGGIGHKCP----TCPTCHKCPVPELLGGP
GKATLTVDTSSSTAYMQLSSLTSEDSAVYFC--
                                         SRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--G 136
                                                                                                                               LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRAPFVCSVVHEGLHNHHVEKSISRPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TFRVVSALPIQHQDWMSGKEFKCKVNNKALPSPIEKTISKPKGLVRKPQVYVMGPPTEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGTW-----TCTVLQ--NQKKVEFKIDI-----VPCPAPEPKSCDKTHTC--PELLGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TEQTVSLTCLTSGFLPNDIGVEWTSNGHIEKNYKNTEPVMDSDGSFFMYSKLNVERSRWD
                                                                                                                                                                             Conservative
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58.6%;
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Pred. No. 1.9e-42;
:8: Mismatches 53;
                                                                                                                                                                                                Score 825; DB 2;
Pred. No. 8.2e-42;
                                                                                                                                                                             Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-Apr-1994 #text_change 16-Jul-1999
                                                                                     -VKQRPGEGLEWIGWIYPGSGNTKYNEKFK 65
                                                                                                                                                                                                                     Length 446;
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  ARGGKFAMDYWG
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A;Molecule type: DNA
A;Residues: 1-326 <BRU>
A;Residues: 1-326 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Accession: C25941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig gamma-1 chain C region - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07
C;Accession: PS0017; C25941
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A; Residues: 220-326 <BR2>
C; Genetics:
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Best Local Similarity
Matches 163; Conserv
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473-482, 1988
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                             180
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 NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG
                                                     RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTK
                                                                                                                                                                                              LVKGYFPEPVTVTWNSGALSSGVHTFPAV------LQSGLYTLTSSVTV-PSSTWPS
                                                                                                                                                                                                                          LLQG---QSLTLTLESPPGSS-----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
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                           RSVSELPILHQDWLNGRTFRCKVTSAAFPSPIEKTISKPEGRTQVPHVYTMSPTKEEMTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
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                                                                                                                                                                                                                                                                                                                                       immunoglobulin C region; immunoglobulin
                                                                                                                                                                                                                                                                                                          immunoglobulin homology <IMM>
                                                                                                                                                                   -TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG------PSV
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                    30.5%; Score 823.5; DB 2; 50.0%; Pred. No. 6.9e-42; tive 53; Mismatches 55;
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A;Title: Immunoglobulin gamma-1 heavy chain gene: struct A;Reference number: A26234; MUID:80202559; PMID:6789752 A;Contents: MOPC 31C A;Accession: A26234
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A; Residues: 1-329 <BRU>
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A;Accession: A02159
A;Molecule type: DNA
A;Residues: 1-324 <HON>
A;Cross-references: GB:J00453
A;Cross-references: was determined from the germline
A;Note: the sequence was determined from the germline
A;Note: Lys-324 is removed posttranslationally
R;Obata, M.; Yamawaki-Kataoka, Y.; Takahashi, N.; Kata
Gene 9, 87-97, 1980
                                                                                                                                                                                                             R;HOnjo, T.; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, Cell 18, 559-568, 1979.

A;Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gammal che A;Reference number: A02159; MUID:80045036; PMID:115593
                                                                                                                                                                                                                                                                                                                       Ig gamma-1 chain C region, secreted form - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Mar.1980 #sequence revision 24-Sep-1981 #text_change 16-Jul-1999 C;Date: 31-Mar.1980 #sequence revision 24-Sep-1981 #text_change 16-Jul-1999 C;Accession: A02159; A26234; A26236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X07189; NID:g57602; PIDN:CAA30169.1; PID:g663228 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin C;Keywords: immunoglobulin F;20-84/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Brueggemann, M.; Delmastro-Galfre, P.; Waldmann, H.; Calabi, Eur. J. Immunol. 18, 317-319, 1988
A;Title: Sequence of a rat immunoglobulin gamma-2c heavy chain A;Reference number: S00847; MUID:88166903; PMID:3127222
A;Accession: S00847
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 23-Jul-1999
C;Accession: S00847
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58.5%;
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Pred. No. 7.5e-42;
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                            N.; Kataoka,
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                              Shimizu,
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gene: structural

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Ig gamma-2b chain - mouse (house mouse) (;Speciles: Mus musculus (house mouse) (;Speciles: Mus musculus (house mouse) (;C;Speciles: Mus musculus (house mouse) (;C;Speciles: Musculus (House mouse) (1-Dec-2000 #text change 01-Dec-2000 C;Accession: $25057; A02157; \overline{A}26235; A26233; A33598 R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, submitted to the EMBL Data Library, July 1992 A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop A;Reference number: $25057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Complex: An immunoglobulin necesses, such as IGA and IgM, the subain disulfide bonds. In some cases, such as IGA and IgM, the such as IGA and I
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F;311-200/Domain: immunoglobulin homology <IM2>
F;311-200/Domain: immunoglobulin homology <IM3>
F;237-304/Domain: immunoglobulin homology <IM3>
F;27-82,138-198,244-302/Disulfide bonds: #status experimental
F;102/Disulfide bonds: interchain (to light chain) #status experimental
F;104,107,109/Disulfide bonds: interchain (to heavy chain) #status experimental
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A;Introns: 1/1; 98/1; 111/1; 218/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Evolution of immunoglobulin subclasses. Primary structure of a mur. A;Reference number: A26237; MUID: 78242288; PMID: 98524
A;Contents: annotation; MOPC 21
A;Note: this is the final paper in a series reporting the protein sequence, A;Note: there are a number of differences from the sequence shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 170-275,'D',277,'D',279-322 <ROG>
A;Cross-references: GB:V00795; NID:G51830; PIDN:CAA24176.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Rogers, J.; Clarke, P.; Salser, W.
Nucleic Acids Res. 6, 3305-3321, 1979
A;Title: Sequence analysis of cloned cDNA encoding part of an A;Reference number: A26236; MUID:80012837; PMID:113776
A;Contents: MOPC 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;174/Binding site: carbohydrate (Asn) (covalent) #status experimental
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LW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLT 142

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A;Molecule type: DNA
A;Residues: 138-172, P',174-189,'FP',193-376,'T',378-474 <TU2>
R;Ollo, R; Rougeon, F.
Nature 296, 761-763, 1982
A;Title: Mouse immunoglobulin allotypes: post-duplication divergence A;Reference number: A26233; MUID:82173203; PMID:6803173
A;Contents: b allele
A;Accession: A26233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F;157-222/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 138-172, 'p',174-189, 'FP',193-376, 'T',378-474 <TU1>
A;Note: Lys-474 is probably removed postcranslationally
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner,
Science 206, 1303-1306, 1979
A;Title: Sequence of the cloned gene for the constant region of A;Reference number: A26232; MUID:80081502; PMID:117549
A;Accession: A26232
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A;Title: Structure of the constant and 3' untranslated A;Reference number: A26235; MUID:80081501; PMID:117548
A;Contents MPC II
      В
                                                                                                                                                                                                                                                                                 F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/bisulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; I. J. Biol. Chem. 269, 12345-12350, 1994
A;Title: O-glycosylation in hinge region of mouse immunoglobulin G2b A;Reference number: A53598; MUID:94216359; PMID:7512967
A;Accession: A53598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
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A;Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474
A;Cross_references: GB:U00461
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A;Residues: 138-161, 'L',163-189, 'FP',193-474 <YAM:
A;Cross-references: GB:J00461
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <FIS>
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A; Accession: A02157
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                                                                                                                                                                                                                                                                                                                                                                                                                   ;236-257/Region: hinge
;281-350/Domain: immuno
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                                                                                                                                                               Similarity
GASVKMSCKASGYTFITYVMHW-----VKQKPGQGLEWIGYINPNKDGTKFNEKFKGKAT
                                                                    GDTVELTCTASQKKSIQF--HWKNSNQIKILGNQG----SFL--TKGPSKLNDRADSRRS
                                                                                                                                                                                                                                                          site: carbohydrate (Asn) (covalent)
                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is shown
                                                                                                                                                            30.3%;
                                                                                                                                  66;
                                                                                                                              Score 818; DB 1; I
Pred. No. 2.3e-41;
6; Mismatches 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  untranslated; PMID:117548
                                                                                                                                                                                         DB 1; Length 474;
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A;Residues: 1330 **OLL>
A;Rote: the sequence was determined from the germline gene A;Note: Ly8-330 is removed posttranslationally
R;Note: Ly8-330 is removed posttranslationally
R;Dourgois, A; Fougereau, M; Rocca-Serra, J.
Eur. J. Biochem. 43, 423-435, 1974
A;Title: Determination of the primary structure of a mouse IgG2a
A;Reference number: A32659; MUID:7417517; PMID:4831970
A;Contents: annotation, myeloma protein MOPC 173
A;Note: this is one paper in a series reporting the sequence; for A;Note: this sequence differs from that shown at a number of posi R;de Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A;Title: Determination of the primary structure of a mouse gammaG
A;Reference number: A32660; MUID:73056887; PMID:4565406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB.V00798; NID:g51835; PIDN:CAA24178.1; PID:g1 R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T. Nucleic Acids Res. 9, 1365-1381, 1981 A;Title: The complete nucleotide sequence of mouse immunoglobulin A;Reference number: A32657; MUID:81198976; PMID:6262729 A;Accession: A32657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1980 #sequence revision 01-Sep-1981
C;Accession: A02152, A32657; A32658
R;Sikorav, J.L.; Auffray, C.; Rougeon, F.
Nucleic Acids Res. 8, 3143-3155, 1980
A;Title: Structure of the constant and 3' untransla A;Reference number: A02152; MUID:81076554; PMID:677
                                                                                                                                                                                                                                                                                                                                                     A;Note: the sequence was determined from the germline gene R;Ollo, R.; Auffray, C.; Morchamps, C.; Rougeon, F. Proc. Natl. Acad. Sci. U.S.A., 2442-2466, 1981
A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests A;Reference number: A32658; MUID:81223894; PMID:6787604
A;Accession: A32658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A02152;
A; Accession: A02152
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A; Residues: 1-330 < YAM>
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annotation;
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MOPC 173,
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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 118-267, 'E', 269-328, 'G', 330-334 < DOG>
C; Comment: Lys-335 is removed posttranslationally.
C; Comment: The sequence differs from that of the a allele, from BALB/c mice, at 15% of t C; Comment: The sequence differs from that of the consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobuff; 20-84/Domain: immunoglobulin homology <IM1>
F; 20-84/Domain: immunoglobulin homology <IM2>
F; 142-211/Domain: immunoglobulin homology <IM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: A02153; A32656
R;Schreier, P.H.; Bothwell, A.L.M.; Mueller-Hill, B.; Baltimore, Proc. Natl. Acad. Sci. U.S.A. 78, 4495-4499, 1981
A;Title: Multiple differences between the nucleic acid sequences a.Deference number: A02153; MUID:82037861; PMID:6170065
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglo F;20-84/Domain: immunoglobulin homology <IM1>
F;98-113/Region: hinge
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G2MSAB
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F;243-310/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;15/D1sulfide bonds: interchain (to light chain) #status experimental
F;27-82,144-204,250-308/Disulfide bonds: #status experimental
F;27-82,144-204,250-308/Disulfide bonds: #status experimental
F;107,110,112/Disulfide bonds: interchain (to heavy chain) #status exp
                                                                                                                                                                                                                                                                                                                                                                        R;Dognin, M.J.; Lauwereys, M.; Strosberg, A.D.
Proc. Natl. Acad. Sci. U.S.A. 78, 4031-4035, 1981
A;Title: Multiple amino acid substitutions between murine
A;Reference number: A32656; MUID:82037777; PMID:6794027
A;Accession: A32656
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A;Experimental source: strain C57BL/6
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A;Accession: A02153
A;Molecule type: mRNA
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C;Accession: A02153; A32656
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                         ;248-315/Domain: immunoglobulin;15/Disulfide bonds: interchain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPPEEEMTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGTW----TCTVLQ--NQKKVEFKID-----IVPCPAPEPKSCDKTHTCPELLGGPSVF
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immunoglobulin homology <IM2>
immunoglobulin homology <IM3>
immunoglobulin homology <IM3>
ids: interchain (to light chain)
ids: homology interchain)
if interchain (to light chain)
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Pred. No. 8.2e-41;
3; Mismatches 58
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predicted
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,255-313/Disulfide

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Ig gamma-2b chain precursor - mouse C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C;Accession: S01321
R;de Waele, P:; Feys, V:; van de Voorde, A.; Molemans, F:; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1986
Eur. J. Biochem. 176, 287-295, 1986
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A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-475 <DE1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 37
                                                                                                                                                                                                                                                                                                                                                            159-223/Domain:
                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                      Local
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 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GLTANSDT--HLLQG---QSLTLTLESPPGSS----PSVQCRSPRGKNIQGGKTLSVSQ
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                                                                                                                                                                                                                                                30 LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQG-----SFLTKGPSKLNDRAD 81
                                                                                                                                                                                                                                                                                       187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                    29.4%; Score 793.5; DB 2; Similarity 40.0%; Pred. No. 6.5e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                    TLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTF
                                                                                                       LTLTLESPPGSSPSVQ-----CRSPRGKNI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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                                                                                                                                         GKATLTVDKSSSTAYLHLSSLTSEDSAVYFCA---GPRQVGLLPFG-----YWGQG 132
                                                                                                                                                                          SRRSLW----DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
PALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLEPSGPTSTINPCP---
                                                                                                                                                                                                               LARPGASVKLSCKASGYTLTSYGISW-----VKORTGOGLEWIGEIYPGSGNSYFNEKFK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TWERGSLEACSVVHEVLHNHLTTKTISRSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAL-----LQSG-LYTLSS
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                    Ig gamma-2b chain #status predicted <MAT>immunoglobulin homology <IMM>
                               SQLELQDSGTW----TCTVLQ--NQKKVEFKID-----IVPCPAPE 206
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                                                                                                                                                                                                                                                                                  58; Mismatches 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 801; DB 1;
Pred. No. 1.5e-40;
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A;Introns: 98/1; 109/1; 216/1
C;Superfamily: immunoglobulin
C;Keywords: immunoglobulin
F;20-84/Domain: immunoglobuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-0un-1990 #sequence revision 07-0un-1990
C;Accession: PS0019; D25941
R,Brueggemann u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-322 <BRU>
R;Residues: 1-322 <BRU>
R;Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold,
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A;Title: Immunoglobulin heavy chain locus of the rat: striking
A;Reference number: A25941; MUID:86287397; PMID:3016742
A;Recession: D25941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 216-322 <BR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Brueggemann, M.
Gene 74, 473-482, 1988
A;Title: Evolution of the rat immunoglobulin gamma heavy-chain
A;Reference number: PS0017; MUID:89232738; PMID:3149946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local
308
                                      418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS0019
                                                                                                                                                                                                                                                                                      ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                         LVKGYFPEPVTVTWNSGALSSGVHTFPAV-----LQSGLYTLTSSVTV-PSSTWSS
                                                                                                                  YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL 417
                                                                                                                                                                                                                                                                                                                                                    QAVTCNVAHPASSTKVDKKIVPREC---NPCGCTGSEV-----SSVFIFPPKTKDVLT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLQG---QSLTLTLESPPGSS----PSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PKSCDKTHTC--PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
HNHHTEKSLSHSPG
                                      HNHYTQKSLSLSPG
                                                                                  YPPDIYTEWKMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKETWQQGNTFTCSVLHEGL
                                                                                                                                                                         WLNGKTFKCKVNSGAFPAPIEKSISKPEGTPRGPQVYTMAPPKEEMTQSQVSITCMVKGF
                                                                                                                                                                                                                  WINGKEYKCKVSNKALPAPIEKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGF
                                                                                                                                                                                                                                                               ITLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNSTLRSVSELPIVHRD
                                                                                                                                                                                                                                                                                                                                                                                         ---TCTVLQ--NQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKFKDTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGIVRAPQVYILSPPPEQLSRKDVSLTCLAVGFSPEDISVEWTSNGHTEENYKDTAPVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- PCKECHKCPAPNLEGGPSVFIFPPNIKDVLMISLTPKVTCVVVDVSEDDPDVQISWFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.3%;
                                      431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 792.5; DB 2;
Pred. No. 4.7e-40;
Mismatches 72;
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A;Accession.
A;Molecule type: DNA
A;Residues: 1-327 <SYM>
A;Cross-references: EMBL:X16702
A;Cross-reacuence was determined
                                                                                                       A;Gene: Ig CH gamma 2, A;Introns: 99/1; 112/1, 219/1
A;Introns: 99/1; 112/1, 219/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; immunoglobulin; membrane protein
C;Keywords: glycoprotein; immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: This protein is expressed on most thymocytes, on a subset of C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication; glycoprotein? T-cell; triansmembrane protein F;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT: F;1-371/Domain: extracellular #status predicted <EXT>
F;9-86/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Alternate names: T-cell surface antigen T4/Leu 3
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: C32722
R;Camerini, D.; Seed, B.
                                                                                                                                                                                                                                 A; Note: the sequence was C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                     R;Symons, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 441-550, 1989
A;Title: Structure of bovine immunoglobulin A;Reference number: S06610; MUID:90097956; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig gamma-2 chain C region (clone 32.2) - bovine (fragment) C;Specides: Bos primigenius taurus (cattle) C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change C;Accession: S06611; B31303
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F;180-293/Domain: immunoglobulin homology <IM3>
F;180-293/Domain: immunoglobulin homology <IM3>
F;296-347/Domain: immunoglobulin homology <IM4>
F;372-395/Domain: transmembrane #status predicted <IM4>
F;372-395/Domain: intracellular #status predicted <IM7>
F;396-432/Domain: intracellular #status predicted <IM7>
F;16-84,130-159,303-345/Disulfide bonds: #status predicted
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell surface N; Alternate nam
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A; Residues: 1-432 < CAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A32722;
A; Accession: C32722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A CD4 domain important for HIV-mediated syncytium formation lies A;Reference number: A32722; MUID:90182664; PMID:2107024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M31134
  Query Match
Best Local S
Matches 146
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Best Local Similarity
Matches 152; Conserv
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                                                                                           /Binding site:
                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVVLGKKGDTVELTCTASOKKNTOFHWKNSNQIKILGIQGLFLTKGPSKLSDRADSRKSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGSSPSVKCRSPGGKNIQGGRTISVPQLERQDSGTWTCTVSQDQKTVEFKIDIV
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    Conservative
                                                                                           carbohydrate (Asn)
                   28.6%;
57.0%;
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antigen T4/Leu
                        Score 774; DB 2;
Pred. No. 6e-39;
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Pred. No. 9.4e-40;
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    Mismatches
                                                                                        (covalent) #status predicted
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                                                                                                                                                                                                                                                       germline
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                                           Length 327;
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  14;
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Gaps
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A;Reference number: A46254; A;Accession: A46254 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-459 <HAG>

CD4 precursor

;Species: Oryctolagus cuniculus (domestic rabbit);Date: 21-Sep-1993 #sequence_revision 18-Nov-1994

#text_change

21-Jan-2000

Recker,

D.P.; human

Kindt,

T.J.

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immunodeficiency

≤.

A; Note: sequence extracted C; Superfamily: T-cell surfa

A;Cross-references: GB:M92840; NID:g164871; PIDN:AAA31198.1; A;Note: sequence extracted from NCBI backbone (NCBIN:112732,

PID: 9164872 NCBIP: 112733)

surface glycoprotein

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                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-180 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Heidmann, O.; Rougeon, F.
Nucleic Acids Res. 10, 1535-1545, 1982
A;Title: Molecular cloning of rabbit gamma
A;Reference number: I46732; MUID:82174328;
A;Accession: I46732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig gamma heavy chain constant region -
[;Species: Oryctolagus cuniculus (domes
C;Date: 14-Feb-1997 #sequence_revision
C;Accession: I46732
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Matches 124
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                                                                                                                                                                                                                                                                                    Similarity
                                                              EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
                                                                                                                                                   PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
                                                                                                                                                                                                 DDPEVQFTWYINNEQVRTARPPLREQQFNSTIRVVSTLPIAHQDWLRGKEFKCKVHNKAL 61
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                                                                                                                                 PAPIEKTISKARGOPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISVEWEKNGKAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFTCNVAHPASSTKVDKAVGVSSDCSKPNNQHCVRE-----PSVFIFPPKPKDTLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWTCTVLQ--NQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLM
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                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (domestic rabbit
                                                                                                                                                                                                                                                                                   Score 702; DB 2;
Pred. No. 5.6e-35;
                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain |
PMID:6280149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change
                                                                                                                                                                                                                                                                                                  Length 180;
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RBSULT 43
330193
T-cell surface glycoprotein CD4 - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Accession: S30193
R,Milde, K.F.; Conner, G.E.; Mintz, D.H.; Alejandro, R.
Biochim. Biophys. Acta 1172, 315-318, 1993
A;Title: Primary structure of the canine CD4 antigen.
A;Reference number: S30193; MUID:93192324; PMID:7916632
A;Accession: S30193; MUID:93192324; PMID:7916632
A;Accession: S30193; MUID:93192324; PMID:7916632
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C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-432 <MIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                Keywords: glycoprotein 202-311/Domain: immunoc
                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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                         183 TCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKFKDTLMISRTP 242
                                                                           120 GSSSGSSNIRLLQGQQLTLTLENPSGSSPSVQWKGPGNKSKHGGQNLSLSWPELQDGGTW 179
                                                                                                                        128
                                                                                                                                                                                                                                                                                                                             tch 21.5%;
al Similarity 32.8%;
170; Conservative 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230
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180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 SAQSWVSFSLEDRKVSVQKILP---DLKIQMSKGLPLS---LTLPQALHRYAGSGNLSLT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 QDSGTWTCTV-LQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKFKDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 LHODWLNGKEYKCKVS-NKALPAPIEKTISKAKGOPREPOVYTLPPSRDELT-KNOVSLT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 LMISRTPEVTCVVVDVSHEDPEV--KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV 293
                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                         12 LVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTK 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 22.3%; Score 601.5; DB 2; Similarity 41.9%; Pred. No. 1.6e-28; 53; Conservative 47; Mismatches 98;
                                                                                                  -----NSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW 182
                                                                                                                                                            GSSRLKHRVESKKNLWDOGSFPLVIKDLEVADSGIYFCDT-DKRQEVELLVFNLTAKWDS 119
                                                                                                                                                                                    GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVELLVFRLTANPNTRLLHGQSLTLTLEGPSVGSPSVQWKSPENKIIETGPTCSMPKLRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILGNQG----SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
TCIISQSQKTVEFNINVLVLAF---QKVSNTFYARE--GDQVEFSFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QDSGTWSCHLSFQDQNKLELDIKIIVLGFPKASA-----TVYKKEGEQVEFSFP-----
                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                               67;
                                                                                                                                                                                                                                                                                                                           Score 581.5; DB 2;
Pred. No. 2.3e-27;
7; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                 Length 432;
                                                                                                                                                                                                                                                                                                                               Indels 129;
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221
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A;Status: preliminary A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-249 < KHA> A;Cross-references: EMBL;X81696 C;Superfamily: immunoglobulin C region; immunoglobulin homology	Status: prel Molecule typ. Residues: 1- Cross-refere Superfamily:	02222:
A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M. 1. 229, 54-60, 1995 Ture of abnormal heavy chains in human heavy-chain-deposition disease ber: \$69339; MUID:95262687; PMID:7744049	Reference nu	2 2 2 E 2 C
VHIII-D-JH-CH3 region - human) sapiens (man) 1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000	RESULT 45 S69340 Ig heavy chair C;Species Hom C;Date: 28-Oct	k o H o o o
CSVMHEGLHNHYTQKSLSLSPG 218	197	뫄
SVMHEALHNHYTQKSLSLSPG 431	410	ð
LTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSRWQQGNVFS 196	Db 137	U 10
13	94	
VLTVLHQDWLNGKEYKCKVSNKALFAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVS 349	290	n
21.3%; Score 574.5; DB 2; Length 218; milarity 77.5%; Pred. No. 2.6e-27; Conservative 3; Mismatches 12; Indels 17; Gaps 1;	Query Match Best Local Simi Matches 110;	
A;Status: preliminary A;Molecule type: protein A;Residues: 1-218 <bul> C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;132-199/Domain: immunoglobulin homology <imm></imm></bul>	Keywords: he Keywords: he Keywords: he	#00××
<pre>Weiss, D.T.; Solomon, A. d. Sci. U.S.A. 87, 6542-6546, 1990 globulin heavy-chain-associated amyloidosis. ber: A36040; MUID:90370821; PMID:2118650</pre>	;;Eulitz, M.; roc. Natl. Ac ;Title: Immur ;Reference nu ;Accession: A	
o sablass (man) 11990	;Date: 16-Nov ;Accession: F	000
V-III region (ART) - human (fragments)	ESULT 44 36040 heavy chair	מ של או
SSLNVSSPVVIKSWPKFLAITLGGILGLLLLIGLCVFC 412	Db 375	ы
SALPDPPAASALPAALAVISFLLGLGLGVAC 506	Qy 476	0
TSPELTLSLNLKEQAAKVSK-QQKLVWVVDPEGGTWQCLLSDKDKVLLA 374	Db 327	В
NHYTOKSLSLSPGLOLDETCAEAQDGELDGLWTTDPPRASALPAPPTGSALPDPQTA 475	Qy 419	0
YQEV TVVMRANSSQNNL-TCEVLGP 326	Db 302	п
SRWQQGNVFSCSV	Qу 359	0
Ľ	Db 249	п
KTISKA	Qy 301	0
ISFEDENLVGELRWQAQGAS	Db 222	п
VHNAKTKPREEQYNSTYRVVSVLTVLHQDW	Qy 243	0

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RESULT 47

A27449

A27449

T-cell Surface glycoprotein CD4 precursor - rat

T-cell Surface glycoprotein CD4 precursor - rat

N;Alternate names: W3/25 antigen

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 21-Jan-2000

C;Accession: A27449; A35433

R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A.F.

Proc. Natl. Acad. Sci. U.S.A. 84, 1649-1653, 1987

A;Title: Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: eviden A;Reference number: A27449; MUID:87175535; PMID:3104900

A;Accession: A27449; MUID:87175535; PMID:3104900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig gamma-1 chain C region (15C5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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S14236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Construction and characterization of a recombinant murine monoclonal A;Reference number: S14236; MUID:91006173; PMID:2209622 A;Accession: S14236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, Eur. J. Blochem. 192, 767-775, 1990
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                   A; Molecule type: mRNA
A; Residues: 1-457 < CLA>
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A; Residues: 1-152 < VAN>
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Best Local
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Best Local Similarity
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e-references: GB:M15768; NID:g203387;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                               RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYTIPPPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- LPSAIHFWGQGTRVIVSSGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDSVRGRFTISRDNSENQLYLQMNSLTAEDTAVYYCAKDVGSVIH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVEVHNAKTKPREEQYNSTYRVVSVLT----
                                                                                                                                                                                                                                                                                                                        LSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KALPAPIE-----KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.9%; Score 566; DB 2; 61.6%; Pred. No. 5.4e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.2%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 572.5;
Pred. No. 4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4e-27;
PIDN:AAA40901.1; PID:g203388
                                                                                                                                                                                                                                                                                                                          151
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                                                                                            antigen: evidence
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                                                                                                                                                                                                                                                                                                                                                                                                                                        400
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R;Davis, S.J.; Ward, H.A.; Puklavec, M.J.; Willis, A.C.; J. Biol. Chem. 265, 10410-10418, 1990
A;Title: High level expression in Chinese hamster ovary of A;Reference number: A35433; MUID:90285164; PMID:2113054
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                       296
                                 356
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                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNRGVPFRHL--LLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                KTILGYKNKLLIKGSLELYSRFDSRKNAWERGSFPLIINKLRMEDSQTYVCELENKKEEV
                                                                                                                                                                                                                                                                                                                                                                                                IKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                      MCRGFSFRHLLPLLLLQLSKLLVVTQGKTVVLGKEGGSAELPCESTSRRSASFAWKSSDQ
----PQVSLQFAGSG----NLTLT---LDR-GILYQEVNLVVMKVTQPDSNTLTCEVM
                                 GFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM 413
                                                                   OSWITTSLKNOKVS-----VOKSTSNPKFOLSE----TLP-----
                                                                                                       QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVK 355
                                                                                                                                                                                                                   DSGIWNCTVTLNQKKHSFDMKLSVL-----GFASTSITAYKSEGESAEFSFP-----
                                                                                                                                                                                                                                                   DSGTWTCTVLQNQKKVEF--KIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDT
                                                                                                                                                                                                                                                                                        ELWVFRVTFNPGTRLLQGQSLTLILDSNPKVSDPPIECKHKSSNIVKDSKAFSTHSLRIQ
                                                                                                                                                                                                                                                                                                                          QLLVFGLTANSDTHLLQGQSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQ 177
                                                                                                                                           ------KAEKAPSS----
                                                                                                                                                                             LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 495; DB 2;
Pred. No. 3.3e-22;
7; Mismatches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 457,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cells
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                                                                     ---LTLQI- 285
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 331
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RWMST4

R;Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R. Science 234, 610-614, 1986
A;Title: Isolation and sequence of L3T4 complementary DNA clones: expression A;Reference number: A02110; MUID:87018845; PMID:3094146 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999 C;Accession: A02110; A26038; A39893; A39955; I54564; I69018; A47642 R;Tourvieille, B.; Gorman, S.D.; Field, E.H.; Hunkapiller, T.; Parnes, J.R. T-cell surface glycoprotein CD4 precursor - mouse N; Alternate names: T-cell differentiation antigen L3T4; T-cell surface antigen A; Accession: A02110 C; Species: Mus musculus (house mouse) ä T4/Leu н cells

A; Molecule type: mRNA A; Residues: 1-457 < TOU>

R;Littman, D.R.; Gettner, Nature 325, 453-455, 1987 A;Title: Unusual intron in A;Cross-references: GB:M13816; NID:g192070; PIDN:AAA37267.1; R;Littman, D.R.; Gettner, S.N. PID: 9309112

in the immunoglobulin domain of 038; MUID:87115821; PMID:3027575

the newly isolated

murine

CD4

F

PID:g50354

in brain

A; Reference number: A26038; A; Accession: A26038

A; Molecule type: mRNA
A; Residues: 1-457 cLIT>
A; Cross - references: GB:X04836; NID:950353; PIDN:CAA28539.1;
A; Cross - references: GB:X04836; NID:950353; PIDN:CAA28539.1;
R; Gorman, S.D.; Tourvieille, B.; Parnes, J.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7644-7648, 1987
A; Title: Structure of the mouse gene encoding CD4 and an unu
A; Reference number: A39893; MUID:88041159; PMID:2823269
A; A; Accession: A39893 unusual transcript

A; Molecule type: DNA A; Residues: 1-25, 'E', 27-457 <GOR>

A;Cross-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; PID: 9387124

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Ig Y heavy chain (7.8S) - duck
N;Alternate names: Ig gamma chain (7.8S)
C;Species: Anas platyrhynchos (domestic
                                                                                    RESULT 49
B46529
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;RE32>
A;Residues: 208-318 <RE2>
A;Cross-references: GB.M36851; NID:g198672; PIDN:AAA39402.1;
A;Cross-references: GB.M36851; Kirszbaum, L.; Maddox, J.; N
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A;Title: Structure and expression of the human and mouse T4 genes.
A;Reference number: A39955; MUID:88097446; PMID:3501122
A;Accession: A39955
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F;220-301/Domain: immunoglobulin homology <IM3>
F;241-457/Product: CD04, brain-specific short form #status predicted
F;321-372/Domain: immunoglobulin homology <IM4>
F;321-372/Domain: immunoglobulin homology <IM4>
F;395-419/Domain: transmembrane #status predicted <INT>
F;420-457/Domain: intracellular #status predicted <INT>
F;42-112,159-188,328-370/Disulfide bonds: #status predicted
F;42-112,159-188,328-370/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Introns: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2
(;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: alternative initiators duplication; glycoprotein; T-cell; trans
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-457/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
F;35-114/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Classon, B.J.; Tsagaratos, J.; Kirszbaum, Immunogenetics 23, 129-132, 1986
A;Title: The L3T4 antigen in mouse and the A;Reference number: A47642; MUID:86166694; A;Accession: A47642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. Rev. 100, 109-127, 1987
A;Title: L3T4 and the immunoglobulin gene superfamily: New relationships between
A:Reference number: I54564; MUID:88152875; PMID:3326818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: the cited GenBank accession number, J03564, is not in R;Parnes, J.R.; Hunkapiller, T. Immunol. Rev. 100, 109-127, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M36850; NID:g198670; A;Accession: I69018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-457 < RES>
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A;Residues: 25-457 <MAD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                  LODSGIWICTVLONOKK 192
                                                                                                                                                                                                                                                                                                                                                          EVOLLVEGLTANSDTHLLOGOSLTLTLES-PPGSSPSVQCRSPRGKNIQGGKTLSVSQLE 175
                                                                                                                                                                                                                                                                                                        EVELWVFKVTFSPGTSLLQGQSLTLTLDSNSKVSNPLTECKHKKGKVVSGSKVLSMSNLR 179
                                                                                                                                                                                                                                                                                                                                                                                                                   KILGQHGKGVLIRGGSPSQF-DRFDSKKGAWEKGSFPLIINKLKMEDSQTYICELENRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KILGNQG-SFLTKG--PSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCRAISLRRLLLLLLQLSQLLAVTQGKTLVLGKEGESAELPCESSQKKITVFTWKFSDQR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WARGALEEH-FITATOTTTEVATOGNIKAATÖKKEDLAETLELTELTVEVÄKRIÖLHMIKARNÖI 23
                                                                                                                                                                                            VQDSDFWNCTVTLDQKK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 475; DB 1; Length 457; Pred. No. 5.1e-21; Mismatches 55; Indels
        duck)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sheep equivalent PMID:3082751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN: AAA39401.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (covalent) #status predicted
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Mackay, C.R.
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R;Amemiya, C.T.; Haire, R.N.; Litman, G.W.
Nucleic Acids Res. 17, 5388, 1989
A;Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin
A;Reference number: S04845; MUID:89345103; PMID:2503814
                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain precursor - African clawed frog (fragment) C;Specias: Xenopus laevis (African clawed frog) C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999 C;Accession: S04845; S05695
                                                                                                                                                                             A; Reference number: A; Accession: S05695
                                                                                                                                                                                             submitted to the EMBL Data Library, April 1989 A; Reference number: S05695
                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-549 <AME>
A;Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Keywords: immunoglobulin F;37-120/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                           R;Litman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: B46529; S20759
R;Magor, K.E.; Warr, G.W.; Middleton,
J. Immunol. 149, 2627-2633, 1992
                                                                                                                                                                                                                                                                                                                       A; Accession:
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A; Residues: 1-572 < MAG>
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                                                                                                                                                                                                                                                                                                                       S04845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGKNIQGGKTLSVSQLELQDSGTWTCTVLQ-----NQKKVEFKIDIVPCPAPEPKSCDK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FFLYSKMTVPKASWQGGVSYACMVVHEGLPMRFTQRPLQKTPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPMVLTEHFNGTFTASSSLAISTQDWLAGERFTCTVQHEDLPVPLGKSIAKHAGKVTAPY 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSKTYMATSQTNVSREDWKAGKAFTCRVKHPATGGTAQGHARF-----CPGSGAQSCSP 360
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Pred. No. 4e-17;
  Score 402.5;
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  Length 549;
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A;Cross-references: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451 C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin; managence protein F;1-15/Domain: signal sequence #status predicted <SIG>F;16-627/Product: Ig mu chain #status predicted <MAT>F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig mu chain precursor, membrane-bound (clone 201) - human C;Species: Homo sapiens (man) C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change C;Accession: $14683; $08047 R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P. Nucleic Acids Res. 18, 4278, 1990 A;Title: Complete nucleotide sequence of the membrane form of th A;Reference number: $14683; MUID:90332450; PMID:2115996 A;Accession: $14683; MUID:90332450; PMID:2115996
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A; Residues: 1-627 < FRI>
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  THTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 272
                                                                                       LELODSG-----
                                                                                                                             AELPPKVSVFVPPRDGFFGNPRSKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQ
                                                                                                                                                                          LESPPGSSPSVQCR------SPR-----SPR-----
                                                                                                                                                                                                                SVLRGGKYAATSQVLLPSKD---
                                                                                                                                                                                                                                                             LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT 142
                                                                                                                                                                                                                                                                                                      SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WNSGSITSGLKNFPAVLQQSGLFASSSQLTIPLSDWKAKKSFECNVEHKPTSTKVTQKIE
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                                          AEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KP---CKEENG-TFSSRSKVSVPKEDWNSEDSYTCKVTH------PASHTKT
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                                                                                                                                                                                                                                                                                                                                                                                         14.4%; Score 389; DB 2; Length 627;
23.9%; Pred. No. 9.6e-16;
Live 77; Mismatches 167; Indels 1
                                                                                                                                                                                                                  -----VMQGTDEHVVCKVQHPNGNKEKNVPLPVI
                                                                                     -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDK 212
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A;Residues: 1-388 cLIU>
A;Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220
A;Cross-references: GB:J00476; NID:g194875; PIDN:AAA38085.1; PID:g387220
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin cregion; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;1-44/Domain: immunoglobulin homology (fragment) <IM1>
F;81-149/Domain: immunoglobulin homology <IM2>
F;186-254/Domain: immunoglobulin homology <IM3>
F;290-361/Domain: immunoglobulin homology <IM4>
F;200-361/Domain: immunoglobulin homology <IM4>
F;10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA
A;Reference number: A02144; MUID:83117774; PMID:6818553
A;Accession: A02144.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig epsilon chain C region (version 1) C; Species: Mus musculus (house mouse)
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376 YKTTPPVLDSDGS---FFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLSPG 431
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                                          VRSITKTPGQRSAPEVYVFPPPEEE-SEDKRTLTCL1QNFFPEDISVQWLGDGKL1SNSQ
                                                                                                                                                                                                                                                                                                      AQTVLIKE-EGKLASTCSKLNITEQQWMSESTFTCKV--TSQGVDYLAHTRRCPDHEPR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIK 97
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                                                                                EKTISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENN--
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Pred. No. 6.2e-16;
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Ig mu chain C region - human C;Species: Homo sapiens (man) C;Date: 12-Feb-1998 #sequence C;Accession: S37768
R;Harindranath, N.; Donadel,
       Mol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-474 <NEA>
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A;Title: mRNA transcripts initiating within the human immunoglobulin
A;Reference number: S15590; MUID:91252286; PMID:1904154
A;Accession: S15590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Neale, G.A.M.; Kitchingman, G.R. Nucleic Acids Res. 19, 2427-2433,
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;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
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                                                                                                                                                                                                                  GLWTT
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                                                                                                                                                                                 NLWAT
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                                                                                                                                                                                                                                                                                                                                                        VYTLPPSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                                                             TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELQDSG----
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.; Donadel, G.;
111-112, 1993
                                                                                                                                                                                                                  452
                                                     #sequence_revision 12-Feb-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQNGQAVKTH
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23.7%; Pred. No. 9.7e-1...
14.3%; Pred. No. 9.7e-1...
14.3%; Scur. 14.3%; Pred. No. 9.7e-1...
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C region; immunoglobulin homology
                    Sigounas,
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:
                    Notkins,
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R:Patri, S.; Nau, F.
Mol. Immunol. 29, 829-836, 1992
Mol. Immunol. 20, 829-836, 1992
A;Title: Isolation and sequence of a cDNA
A;Reference number: \$25705; MUID:92342148;

coding for the pMID:1635560

immunoglobulin mu chain

of the

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-592 <PAT>

A; Accession: S25705

A;Cross-references:

EMBL:X59994; NID:g1269; PIDN:CAA42611.1; PID:g1270

C;Species: Ovis orientalis aries, Ovis ammon aries C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 C;Accession: S25705

(domestic sheep)
#text_change 23-Jul-1999

Ig mu chain -C;Species: Ovi

sheep

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F;127-199/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;344-415/Domain: immunoglobulin homology <IMM3>
F;144-115/Domain: immunoglobulin homology <IMM4>
F;144/Disulfide bonds: interchain (to light chain) #status predicted F;28-88,134-197,244-303,351-413/Disulfide bonds: #status predicted F;46,209,272,279,440/Binding site: carbohydrate (Asn) (covalent) #status predicted F;214,452/Disulfide bonds: interchain (to heavy chain) #status predicted F;291/Disulfide bonds: interchain (to mu chain in another subunit) #statu
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A;Residues: 1-453 <NAFS
A;Cross-references: EMBL:X67301; NID:g38407; PIDN:CAA47714.1; PID:g38408
A;Experimental source: cell line Ab 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIIKNLKIEDSDTYICEVED----QKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
LTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTG
                                      LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                     REQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPGRYFAHSI
                                                                                                                           RDELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSK
                                                                                                                                                                        PNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPDVYLLPPA
                                                                                                                                                                                                                 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPS
                                                                                                                                                                                                                                                            ----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRONGEAVKTHTNISESH
                                                                                                                                                                                                                                                                                                  GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
                                                                                                                                                                                                                                                                                                                                                 TTYKVTSTLTIKESDWLSQSMFTCRV--DHRGLTFQQNASSMCVPDQDTAIR-
                                                                                                                                                                                                                                                                                                                                                                                                                                    SVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQAEAKESGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPSVQCR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVAVGCLAQDFLPDSITFSWKYKNNSDISSTRG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.1e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 385; DB 2;
Pred. No. 1.1e-15
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                                          431
434
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RESULT
MHHUM
       R;Rabbitts, T.H.; Forster, A.; Milstein, C.P. Nucleic Acids Res. 9, 4509-4524, 1981
A;Title: Human immunoclobulin basson and the control of t
                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: S16656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X14939
A;Note: the authors translated the codon AAC for residue A;Note: the sequence of residues 1-432 was assumed to be A;Accession: S09357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 29-Jan-1993 #sequence revision 23-Aug-1997 #text_change 22-Jun-1999 C;Accession: S16510; S09357; S16656; B26243; A02167 R;Dorai, H.; Gillies, S.D. Nucleic Acids Res. 17, 6412, 1989 A;Title: The complete nucleotide sequence of a human immunoglobulin genomic C-mu A;Reference number: S09357; MUID:8936690; PMID:2505237 A;Accession: S16510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ર્
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                                                                                                                                       A; Molecule type: DNA A; Residues: 1-39, 'L', 41-432, 'GKPTLYNVSLVMSDTAGTCY'
                                                                                                                                                                                                                         A;Reference number: A;Accession: S16656
                                                                                                                                                                                                                                                                                                                                      R; Dorai,
                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X14940 A;Note: the authors translated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-432, 'GKPTLYNVSLVMSDTAGTCY'
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A; Residues: 433-473 < DOR1>
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                                                                                                                A; Cross-references: EMBL: X14940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELT-KNOVSLTCLVKGFYPSDIAVEWESNGOP--ENNYKTTPPVLD--SDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG-QPREPQVYTLPPSR 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYSVLTITEREWLSQSAYTCQVEHNKETFQKNAS-----SSCDATPPSP--IG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTVALGCLARDFVPNSVSFSWKFNNSTVSSERFWTF----PEVLRD-----GLWSASSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQLSLRESASVTCLVKGFAPADVFVQWLQKGEPVAKSKYVTSSPAPEPQDPSAYFVHSIL
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   immunoglobulin heavy chain genes:
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Pred. No. 1.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                      codon AAT for
                                                                                                                                                                                                                                                                                         April . 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <DOR2>
evolutionary comparisons
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   of C-mu,
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F;237-305/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;433-473/Domain: immunoglobulin homology <IMM4>
F;433-473/Domain: immunoglobulin homology <IMM4
F;141/Disulfide bonds: interchain (to light chain) #status experimental
F;28-88,134-197,244-303,351-413/Disulfide bonds: interchain (to heavy chain) #status experimental
F;246,209,272,279/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;214/Disulfide bonds: interchain (to mu chain in another subunit) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 14q32.33-14q32.33
A;Introns: 1/1; 105/1; 217/1; 333/1; 433/1; 471/3
C;Complex: An immunoglobulin heterotetramer subunit consists of
hain disulfide bonds. The IgM subunits associate into disulfide
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; glycoprotein; heterotetramer;
E;21-90/Domain: immunoglobulin homology <IMM1>
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A;Accession: B26243
A;Accession: Lype: DNA
A;Molecule type: DNA
A;Residues: 433-436,'N',438,'E',440-447,'T',449-473 <RAB>
A;Cross-references: GB:KO1310; NID:g184715; PIDN:AAB59422.1;
C;Comment: During differentiation, B lymphocytes switch from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 116
                        57
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                                                                                                   NLWAT
                                                                                                                                                      GLWTT 452
                                                                                                                                                                                                         RYFAHSILTVSEEEWNTGETYTC-VAHEALPNRVTERTVDKS----
                                                                                                                                                                                                                                                     SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELD 447
                                                                                                                                                                                                                                                                                                                                                                                                                                            TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AELPPKVSVFVPPRDGFFGNPRKSKLICQATGFSPRQIQVSWLREGKQVGSGVTTDQVQA
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                                                                                                                                                                                                                                                                                                                                                        VYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVLD--SDG
                                                                                                                                                                                                                                                                                                                                                                                                                 TNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPKGVALHRPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRONGEAVKTH
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                                                                                                                                                                                                                                                                                                          VYLLPPAREQLNLRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.1%; Score 381; DB 1; 23.9%; Pred. No. 2.1e-15; vative 77; Mismatches 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VMQGTDEHVVCKVQHPNGNKEKNVPLPVI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKT
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Ig epsilon chain C region - mouse (fraç C;Species: Mus musculus (house mouse) C;Date: 06-Jan-1995 #sequence_revision

- mouse (fragment)

06-Jan-1995

#text_change 24-May-2001

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A; Decause gran
A; Molecule type: mRNA
A; Residues: 1-190,'S',192-414,'V',415-452 <HAR>
A; Residues: 1-190,'S',192-414,'V',415-452 <HAR>
A; Cronn-references: EMBL:X67292; NID:g38405; PIDN:CAA47708.1;
                                                                                                                           A; Molecule type: DNA
A; Residues: 1-39, 'L', 41-452 < DOR2>
A; Cross-references: EMBL:X14940
R; Harindranath, N.; Donadel, G.; Sigounas,
Mol. Immunol. 30, 111-112, 1993
A; Title: Comparison of complete nucleotide
A; Reference number: S37767; MUID:93109369;
A; A; Accession: S37767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Datc: 29-Jul-1981 #sequence revision 23-Aug-1997 #text change 22-Jun-1999
C;Accession: S09357; S16656; S37767; A26243; A26244; I37749; I37750; A02162; R;Doral, H.; Gillies, S.D.
Nucleic Acids Res. 17, 6412, 1989
A;Title: The complete nucleotide sequence of a human immunoglobulin genomic C
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                                                                                                                                                                                                                                                                                                                     A;Reference number: A;Accession: S16656
                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, A; Reference number: S16656
                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X14940 A;Note: the authors translated the codon AAT for
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                                                                                                          A;Status: preliminary
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A;Accession: S09357
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: S38864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 KPKDTLMISRTPEVTCVVVDV-SHEDPEVKFN------WYVDGVEVHNAKTKPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLEVAKTLWTQRKQFTCQVIHEALQKPRKLEKTISTS 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLS 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEEE-SEDKRTLTCLIQNFFPEDISVQWLGDGKLISNSQHSTTTP-LKSNGSNRGFFIFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---NATTSITSILPVVAKDWIEGYGYQCIVDHPDFPKPIVRSITKTPGQRSAPEVYVFPP
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Pred. No. 2.4e-15;
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                                                                                                                                                        sequence of the human PMID:8417370
                                                                                                                                                                                                                         G.; Notkins, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a human immunoglobulin genomic C-mu PMID:2505237
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                                    PID: 938406
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                                                                                                                                                                           Igm heavy chain
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A; Molecule type: protein
A; Residues: 100-144, 'E', 146-162, 'E', 164, 'E', 166-214, 'G', 216-262, 'D', 264-295, 'D', 297-414, A; Note: all four combinations of the 191-Ser/Gly and 215-Val/Gly polymorphisms have been R; Watanabe, S.; Barnikol, H.U.; Horn, J.; Bertram, J.; Hilschmann, N. Hoppe-Seyler's Z. Physiol. Chem. 354, 1505-1509, 1973
A; Title: The primary structure of a money and structure of a money structure of a mon
                                              F;127-199/Domain: immunoglobulin homology <IMM2>
F;237-305/Domain: immunoglobulin homology <IMM3>
F;237-305/Domain: immunoglobulin homology <IMM4>
F;344-415/Domain: immunoglobulin homology <IMM4>
F;432-452/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain)
                                                                                                                                                                                                                                                                                                              A, Cross-references: GDB:120086; OMIM:147020
A, Map position: 1432.33-1432.33
A, Introns: 1/1; 105/1; 237/1; 433/1
C; Complex: An immunoglobulin heterotetramer subunit consists of hain disulfide bonds. The IgM subunits associate into disulfide C; Superfamily: immunoglobulin C region; immunoglobulin homology C; Keywords: alternative splicing; glycoprotein; heterotetramer; F; 21-90 Domain: immunoglobulin homology cIMU:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Complete amino acid sequence of the mu heavy chain of a human IgM immunoglobulir A;Reference number: A02088; MUID:74005511; PMID:4742735 A;Contentes: annotation; Waldenstrom's macroglobulin Ou, sequence, disulfide bonds, and ca A;Note: this sequence differs from that shown at a number of positions; this sequence has C;Comment: During differentiation, B lymphocytes switch from expression of membrane-bounce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Contents: annotation; Waldenstrom's macroglobulin Gal
A;Note: this sequence has been revised in reference A02162
R;Putnam, F.W.; Florent, G.; Paul, C.; Shinoda, T.; Shimizu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 8, 5983-5991, 1980
A;Title: Cloning of human immunoglobulin mu gene and comparison
A;Reference number: 137748; MUID:81124312; PMID:6450943
A;Accession: I37749
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A;Residues: 298-386;436-452 <DOL>
A;Cross-references: GB:J00257; NID:g185053; PIDN:AAA53508.1;
A;Cross-references: GB:Honjo, T.
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A; Molecule type: DNA
A; Residues: 1-17;105-186;200-259;296-322;339-416,'D',418-452
A; Cross-references: GB: K01310; NID: g184715
A; Croce, C.M.
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R;Takahashi, N.; Nakai, S.; non-
R;Takahashi, N.; Nakai, S.; non-
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Proc. Natl. Acad. Sci. U.S.A. 77, 6027-6031, 1980
A;Title: Cloning and partial nucleotide sequence of human immunoglobulin mu
A;Reference number: A26244; MUID:81077306; PMID:6777778
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A;Residues: 1-17,'BPS',22,'T',24-82,'N',84-90,'Z',92-93,'B',95,'B',97-144,'E',146-162,'E
A;Accession: B02162
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A; Residues: 433-452 <TAK2>
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;Mihaesco, E.; Barnikol-Watanabe, S.; Barnikol, H.U.; Mihaesco, C.; Hilschmann, N.
iur. J. Blochem. 111, 275-286, 1980
;Title: The primary structure of the constant part of mu-chain-disease protein BOT
;Reference number: A02162; MUID:81066716; PMID:6777162
;14/Disulfide bonds: interchain (to light chain) #status experimental
;28-88,134-197,244-303,351-413/Disulfide bonds: #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two identical light linked pentamers.
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RESULT 59
S03186
Ig heavy chain C region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Sep-1999
C;Accession: S03186
R;Haire, R.N.; Shamblott, M.J.; Amemiya, C.T.; Litman, G.W.
Nucleic Acids Res. 17, 1776, 1989
A;Title: Acids Res. 17, 1776, 1989
A;Telescond Xenopus immunoglobulin heavy chain constant region isotype gene.
A;Reference number: S03186
A;Accession: S03186
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-448 <HAI>
A; Cross-references: EMBL: X13779; NID: g64827; PID: g64828
A; Cross-references: EMBL: X13779; NID: g64827; PID: g64828
A; Note: the authors translated the codon TTT for residue 9 as Ser and C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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Best Local S
Matches 112
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Best Local Similarity
Matches 117; Conserv
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                                 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 LIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLL------QGQSLTLT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 13.9%; Score 376.5; DB 1; Similarity 24.1%; Pred. No. 3.6e-15; 12; Conservative 75; Mismatches 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYFAHSILTVSEEEWNTGETYTC-VAHEALPNRVTERTVDKSTG 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP-REPQ 332
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                                                                                                                                                                              ADPLDIQWNDGSITTGIKTMRPVLSDVDGLYTLSSQLTILASEWKNSTYKCKVVHNYTNT
                                                                                                                                                                                                                          ADSRRSLWDQGNFPLIKNLK--IEDSD------
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                                                                             KQEKSLKVLPCMA-----PHVQLFLQSPCMSDAISRAQHENINATLDLLCIINNFY 145
                                                                                                                             KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSP----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VYLLPPAREQUINTRESATITCLVTGFSPADVFVQWMQRGQPLSPEKYVTSAPMPEPQAPG
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                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                        13.8%; Score 374; DB 2; Length 448; 26.8%; Pred. No. 5e-15; ative 57; Mismatches 144; Indels 1
-SVQCRSPRGKNIQGGKTLSVSQLELQDSGTW-----TCTVLQN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 452;
                                                                                                                                                                                                                            -----TYICEV----EDQ 114
                                                                                                                                                                                                                                                                          Indels 118;
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	Query Match 13.8%; Score 373.5; DB 1; Length 476; Best Local Similarity 25.2%; Pred. No. 5.8e-15;
predicted s predicted	', Domain: carboxyl-terminal <ct's lifide bonds: interchain (to light chain) #status predicted 36-199,246-305,353-415/Disulfide bonds: #status predicted 243,258,281/Binding site: carbohydrate (Asn) (covalent) #status sulfide bonds: interchain (to heavy chain) #status predicted sulfide bonds: interchain (to mu chain in another subunit) #status</ct's
entical light (ka) associate into 1 ramer; immunoglob	subunit consists of two id IgA and IgM, the subunits noglobulin homology or; glycoprotein; heterotet hM2> MM2> MM3>
h the correspon	
comparison	202.1; PID:g817972 globulin mu gene and
D:g52344 , R. ted forms o	L.; Wall,
99 L. y alternative	RESULT 60 MHMSM Ig mu chain C region, membrane-bound form - mouse C; Species: Mus musculus (house mouse) C; Date: 31-Oct-1980 #sequence revision 30-Jun-1991 #text_change 22-Jun-1999 C; Accession: A02167; A37517; B02166 R; Barly, P:; Rogers, J:; Davis, M:; Calame, K:; Bond, M:; Wall, R:; Hood, L Cell 20, 313-319, 1980 A; Title: Two mRNAs can be produced from a single immunoglobulin mu gene by A; Reference number: A02167; MUID:80222874; PMID:6771020
	Qy 416 ALHNHYTQKSLSLSPG 431 : :
E 415	Qy 359 PSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHE
Y 358	Qy 301 GKEYKCKVSNKALPAPIEKTISKA-KGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFY :- :- :-
N 300	Qy 249VDVSHEDPEV-KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN
S 248	Qy 190 QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVV-
T 204	Db 146 HGQIKVKWLVNGKQDVSAEASVPTPSKTEDGTYSSSSQLRIL-KGMWNKGTQYSCIVTHT

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A;Molecule type: mRNA
A;Residues: 'N', 169-307,'L',309-342 <KIN>
A;Residues: 'N', 169-307,'L',309-342 <KIN>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;19-80/Domain: immunoglobulin homology <IM1>
F;19-80/Domain: immunoglobulin homology <IM1>
                                                                                                                                                 F;118-186/Domain: immunoglobulin nomology F;223-291/Domain: immunoglobulin homology <IM3>
F;327-398/Domain: immunoglobulin homology <IM4>
F;327-398/Domain: immunoglobulin homology <IM4>

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C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A93442; A99937; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin
A;Reference number: A93442; MUID:83064537; PMID:6292865
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                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: A;Reference number: A90937; MUID:83182019; PMID:6820340 A;Contents: myeloma IR162
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: str. R;Kindsvogel, W.R.; Reddy, DNA 1, 335-343, 1982
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                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A90937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-429 <HEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A93442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                             99,170,240,265,369,419/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145
                     160 GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24
                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SILTVTEEEWNSGETYTCVVGHEALPHLVTERTVDKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGLQLDETCAEAQDGELDGLWTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAREQUALRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSRDELT-KNOVSLTCLVKGFYPSDIAVEWESNGO--PENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASQSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPPRDGFSGPAPRKSKLICEATNFTPKPITVSWLKDGKLVESGFTTDPVTIENKGSTPQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPP----GSSP---SVQCR----SPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSQVLLSPKSILEGSDEYLVCKIH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain LOU/c/Wsl, immunocytoma IR:
ddy, E.P.; Moore, J.M.; Faust Jr.,
  ::
                                                                                  13.7%; Score 370.5; DB 1; 31.5%; Pred. No. 7.7e-15;
                                                               62; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YG-GKNRDLHVPIPAVAEMNPNVNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GKNIQGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --TEGEVNAEEEGFENLWTT
                                                               Indels
                                                                                                                                             (Agn)
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                                                                                                                                             (covalent) #status predicte
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                                                               27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- LRTGGKYLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 439-479 <BE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Contents: a2 allotype A; Accession: A02165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 62
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                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                        local Similarity
                                          148
  188
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                                                                                                                                                                                                                                                                                                                                                                      123;
                                                                                                                                                                                                                                                77
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                                                                                                                                                                                                                                                                                                                             21
QNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                        SVSWLRDGQKVESGVLTKPVEAETKGAGPATFSISSMLTITESDWLSQSLYTCRVDHRGI
                                                                                  -----GKNIQGG-
                                                                                                                                                                  VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR-----
                                                                                                                                                                                                                                             NDRADSRRSLWDQGNFPLIIKNLK------IEDSDTY-ICEVEDQKEEVQLL 121
                                                                                                                                                                                                                                                                                                                           AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                        -SSRTV---RTFPVVKRGDKYMATSQVLVPSKDVLQGTEEYLVCKVQHSNSNRDLR
                                                                                                                                                                                                                                                                                                                                                                                    13.7%;
                                                                                                                          SFPVDSELPPNVSVFIPPRDSFSGSGTRKSRLICQATGFSPKQI 147
                                                                                                                                                                                                                                                                                                                                                                   79;
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HHNATTSITSILPVDAKDWIEGEGYQCRVDHPHFPKPIVRSITKAPGKRSAPEVYVFLPP
                                                       KLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLSPG
                                                                                                                  EEEE--KDKRTLTCLIQNFFPEDISVQWLQDSKLIPKSQHSTTTP-LKYNGSNQRFFIFS
                                                                                                                                                    SRDELTKNQVSLTCLVKGFYPSDIAVEW--ESNGQPENNYKTTPPVLDSDGS---FFLYS
                                                                                                                                                                                                                                                                          QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT-LPP
                                                                                                                                                                                                                                                                                                                                                           --GVITYLIPPSPLD-LYENGTPKLTCLVLDLESEE-NITVTWVRERKKSIGSASQRSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKLASTYSRLNITQQQWMSESTFTCKVTSQGE--NYWAHTRRCSDDEPR---
RLEVTKALWTOTKOFTCRVIHEALREPRKLERTISKSLG
                                                                                                                                                                                                                                                                                                                                                                                                                   LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE
                                                          431
   418
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                                                                                                                                                                                                                                                                                                                                                           262
                                                                                                                                                                             393
                                                                                                                                                                                                                                           322
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F;130-202/Domain: immunoglobulin homology <IMM2>
F;242-310/Domain: immunoglobulin homology <IMM3>
F;242-310/Domain: immunoglobulin homology <IMM3>
F;349-420/Domain: immunoglobulin homology <IMM4>
F;439-479/Domain: immunoglobulin homology <IMM4>
F;439-479/Domain: carboxyl-terminal <CTS>
F;14/Disulfide bonds: interchain (to light chain) #status predicted F;28-99,137-200,249-308,356-418/Disulfide bonds: #status predicted F;46,114,212,261,277,284/Binding site: carbohydrate (Asn) (covelent) F;219/Disulfide bonds: interchain (to heavy chain) #status predicted F;296/Disulfide bonds: interchain (to mu chain in another subunit) #s A;Note: the sequence of residues 1-438 was assumed to be identical with the correspondin C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases to the land IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu F;21_92/Domain: immunoglobulin homology <IMM1> C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Dec-1986 #sequence revision 30-Jun-1991 #te.
C;Accession: A02165; A02164
R;Bernstein, K.E; Alexander, C.B.; Reddy, E.P.; Mage,
J. Immunol. 132, 490-495, 1984 A;Molecule type: mRNA A;Residues: 1-438,'GKPTLYNVSLIMSDTASTCY' <BER> A; Title: Complete sequence of a cloned cDNA encoding rabbit A; Reference number: A02164; MUID:84088930; PMID:6418803 mu chain C region, membrane-bound form - rabbit #text_change R.G. secreted 23-Aug-1997 #status predicted mu-chain #status predicted of V-Ha2

Score 369.5; DB Pred. No. 1e-14;

DB 1;

479;

Mismatches 153;

Indels 161; Length

Gaps

23

76

50

CLARDFLPSSVTFSWSFKNNSEI-

--KTLSVSQLELQDSGTW-----TCTV----L 187

247

207

-SPR--

159

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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kaphain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily; immunoglobulin cregion; immunoglobulin homology (Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin place (Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology <IMM1> F;20-199/Domain: immunoglobulin homology <IMM2> F;234-302/Domain: immunoglobulin homology <IMM4> F;341-412/Domain: immunoglobulin homology <IMM4> F;430-450/Domain: immunoglobulin homology <IMM4> F;430-450/Domain: immunoglobulin homology <IMM4> F;440-450/Domain: immunoglobulin homology <IMM4> F;490-450/Domain: carboxyl-terminal <CTS> F;4/Disulfide bonds: interchain (to light chain) #status predicted F;27-87,133-194,241-300,348-410/Disulfide bonds: #status predicted F;211,449/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F;288/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;McCumber, L.J.; Capra, J.D.
Mol. Immunol. 16, 565-570, 1979
A;Title: The complete amino-acid sequence of a canine mu chain.
A;Reference number: A93131; MVID:80077682; PMID:117299
A;Contents: myeloma protein Moo
A;Accession: A93131
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MHDG
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A;Residues: 1-177 <MCC>
A;Residues: 1-177 <MCC>
R;Masserman, R.L.; Capra, J.D.
Science 200, 1159-1161, 1978
Science 200, 1159-1161, 1978
A;Title: Amino acid sequence of the Fc region of a canine immunoglobulin M: interspecies
A;Reference number: A94246; MUID:78180587; PMID:653360
A;Contents: Moo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig mu chain C region - dog (tentative sequence)
C;Species: Canis lupus familiaris (dog)
C;Date: 13-Jul-1981 #sequence revision 13-Jul-1981 #text_change 31-Mar-2000
C;Accession: A93131; A94246; A02169
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Best Local Similarity
Matches 119; Conserv
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                              106
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                                                                                                                                                                                                                                         22 TVAMGCLARDFLPGSITFSWKYEBLSAINSTRG---
                                                                                                                                                                                                                                                                                           36
                                                                                                                                                                 LIIKNLK-----IEDSDTYI-CEVE----DQKEEVQLLVFGLTANSDTHLL 134
                                                                             QGQSLTLTLESPPGSSPSVQCR------
                                                                                                                                  SVLRGGKYVATSQVFLPSVDIIQGTDEHIVCKVRHSBGBKQKBVPLPVM------
                                                                                                                                                                                                                                                                                           TVELTCTASQ--KKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVDVSHEDPEVKFNWYVDGVEVHNAKT-----KPREEQYNSTYRVVSVLTVLHQDWLNGK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FFDKNVSMSSECSTTPSP---
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                                                                                                                                                                                                                                                                                                                                                      Conservative
                         LTL--PPEVSGFIPPRDAFFGBPRKSQLICQASGFSPRQVWSLRDGKQIESGVT
                                                                                                                                                                                                                                                                                                                                                                         13.7%; Score 369; DB 1; Length 450; 24.1%; Pred. No. 1e-14;
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                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                   139;
                                                                             ---SPR-----GKNIQGGKT 168
                                                                                                                                                                                                                                                                                                                                                Indels 156;
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360	Qy 303 EYKCKVSNKALPAPIEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPS	_
237	TCLVTDLTTYD-SVTISWTRQDGEAVKTHTNISESHPNATFSAVGEASICEDDWDSGE	н
302	QY 243 EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK	_
242	QY 190 -QKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTP	н о
128		н
189	Qy 157SPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN	_
68	18 EAEDRIIKEEEARLSGRDMQVTSQPVIAELPPKVSVFVPPRDGFFGNPRKS	-
156	OY 110 EVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCR	_
15;	Query Match 13.5%; Score 365.5; DB 1; Length 391; Best Local Similarity 28.0%; Pred. No. 1.4e-14; Matches 105; Conservative 65; Mismatches 132; Indels 73; Gaps	
cted	;65-137/Domain: the uncompleted form of the control	יונה ואו ואו וא
smembrane pro	Superfamily: immunoglobulin C region; immunoglobulin; Reywords: duplication; glycoprotein; heterotetramer; 11-41/Domain: pre-C <var></var>	1 111 0 0
	A;Gene: GDB:IGHM A;Cross-references: GDB:120086; OMIM:147020 A;Map position: 14q32.33-14q32.33	מ מ מ
	A;Molecule type: protein A;Residues: 1-391 <bar> C;Comment: This protein has no V region homology or CH1 region. C;Genetics:</bar>	~ ~ ~ ~
mino-acid sequ	7'6 Z. Physiol. Chem. 365, 105-118, 1984 e primary structure of mu-chain-disease protein BOT. Peculiar a number: A02163; MUID:84184186; PMID:6425189 : A02163	די מי מי מי
mann, N.	anabe, S.; Mihaesco, E.; Mihaesco, C.; Barnikol, H.U.; Hilsc	# O (
	RESULT 64 MHHUBT Ig mu heavy chain disease protein (Bot) - human C;Species: Homo sapiens (man) C;Species: 04-Dec-1986 #secuence revision 04-Dec-1986 #text change 16-Jul-1999	K Z H O O
	Db 435 LYNVSLVLSDTAGZ 448	
	Qy 432LQLDETCAE 440	_
434	Db 375 VTSAPMPEPQAPGLYFAHSILTVSEEEMNAGETYTCVVAHESLPNRVTERSVDKSTGKPT	_
431	ļ	_
374	Db 315 ISRPKGVAVHMPSVYVLPPSREQLDLRESATLSCLVTGYSPPDVFVQMVQKGQPVPPDSY	_
376		_
314	Db 255 SWTREENGALKTHTNISESHPNGTFSAMGEATVCVEEWESGEQFTCTVTHTDLPSVLKQT	_
320		_
254	Db 211 -CTSDQPVGISIFTIPPS-FASIFNTKSAKLSCLVTDLATYD-SVTI	п
260	DPEVKF	_
210	158 TNEVZAZAKZSGPTTYKVTSMLTIQEDAWLSQSVFTCKVEHRGLTFQQNASSM	н
200	Qy 169 LSVSQLELQDSGTWTCTWLQNQKKVEFKIDIV	

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RESULT 66
A24976
    Ig mu chain C region (allele b) - mouse C;Species: Mus musculus (house mouse) C;Date: 05-Jun-1988 #sequence_revision (
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F;220-288/Domain: immunoglobulin homology <IMM3>
F;325-396/Domain: immunoglobulin homology <IMM3>
F;325-396/Domain: immunoglobulin homology <IMM4>
F;23-75,122-181,227-286,333-394/Disulfide bonds: #status
F;43,84,167,239,262,417/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin Cregion; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: immunoglobulin homology <IMMI>
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A;Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison A;Reference number: A90966; MUID:84236092; PMID:6329728
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A; Residues: 1-423 <ISH>
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C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change
C;Accession: A02145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 GKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 CEVEDQKEEVQL--LVFGLTAN--SDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQ 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 13.5%; Score 363.5; DB 1; Length 423;
Similarity 29.8%; Pred. No. 2e-14;
03; Conservative 68; Mismatches 114; Indels 61
                                                                                                                                                                                    --FFLYSKLTVDKSRWQQGNVFSCSVMHEALHN-HYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCSKLNITEQQWMSESTFTCRV--TSQGVDYLAHTRRCPDHEPR-----
                                                                                                                                                                                                                                                     QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN--YKTTPPVLDSDGS- 388
                                                                                                                                             QGFFIFSRLEVAKTLWTQRKQFTCQVIHEALQKPRKLEKTISTSLG
                                                                                                                                                                                                                                                                                                                                                                                             TYLIPPSPLD-LYQNGAPKLTCLVVDLESEKNVNVTWNQEKKTSVSASQWY---TKHHN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDPNAFHSTIQLYCFIYGHILNDVSVSWLMDDREITDTL----AQTVLIKE-EGKLAS
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                                                                                                                                                                                                                              EVYVFPPPEEE-SEDKRTLTCLIQNFFPEDISVQWLGDGKLISNSQHSTTTP-LKSNGSN 370
                                                                                                                                                                                                                                                                                                               -----NATTSITSILPVVAKDWIEGYGYQCVVDRPDFPKPIVRSITLPQVSQRSAP 312
                                                                                                                                                                                                                                                                                                                                                KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREP
                                                                                                                                                                                                                                                                                                                                                                                                                                     VFLFPPKPKDTLMISRTPEVTCVVVDV-SHEDPEVKFN------WYVDGVEVHNA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPNRVTERTVDKSTG
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#sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
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C;Accession: A24976
R;Schreier, P.H.; Quester, S.; Bothwell, A.
Nucleic Acids Res. 14, 2381-2389, 1986
A;Title: Allotypic differences in murine mu-genes.
A;Reference number: A24976; MUID:86176735; PMID:3083402
A;Recession: A24976
A;Molecule type: mRNA
A;Residues: 1-455 <SCH>
A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382
A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382
A;Cross-references: GB:X03690; NID:g52381; PIDN:CAA27326.1; PID:g52382
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;346-417/Domain: immunoglobulin homology <IMM>
                         A;Note: the sequence was determined from the germline gene R;Goldberg, G.I.; Vanin, E.F.; Zrolka, A.M.; Blattner, F.R. Gene 15, 33-42, 1981
A;Title: Sequence of the gene for the constant region of the mu A;Reference number: A26239; MUID:82051295; PMID:6795090
A;Accession: A26239
                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Date: 31-Oct-1980 #sequence revision 31-Oct-1980 #text_change 16-Aug-1996
C;Accession: A02166; A26239; A26240; B02039
R;Kawakami, T: Takahashi, N: Honjo, T.
Nucleic Acids Res. 8, 3933-3945, 1980
A;Title: Complete nucleotide sequence of mouse immunoglobulin mu gene and coa;Reference number: A02166; MUID:81076590; PMID:6255422
A;Accession: A02166; MUID:81076590; PMID:6255422
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-455 < KAW>
A;Molecule type: DNA
                                                                                                                                                                                                            A;Cross-references: GB:J00443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig mu chain C region, secreted form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST------DIL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPP----GSSP---SVQCR----SPR-----GKNIQGG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSQVLLSPKSILEGSDEYLVCKIH------YG-GKNKDLHVPIPAVAEMNPNVNVF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---PLIIKNLKIEDSDTY-ICEVEDQKEEVQLLVFGLTANSDTHL----LQGQSLTLTLE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAMGCLARDFLPSTISFTWNYQNNTEVIQGIRTFPT-----LRTGGKYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --TFTIPPSFAD-IFLSKSANLTCLVSNLATYE-TLNISWASOSGEPLETKIKIMESHPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.4%; Score 363; DB 2; 25.3%; Pred. No. 2.3e-14;
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C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobul; plantal protein; heterotetramer; immunoglobulin homology <IRM1>
F;129-201/Domain: immunoglobulin homology <IRM2>
F;239-307/Domain: immunoglobulin homology <IRM3>
F;346-417/Domain: immunoglobulin homology <IRM3>
F;346-417/Domain: immunoglobulin homology <IRM3>
F;446-417/Domain: carboxyl-terminal <CTS>
F;44/Disulfide bonds: interchain (to light chain) #status predicted
F;28-89/Disulfide bonds: #status experimental
F;28-89/Disulfide bonds: #status experimental
F;46,211,243,281,442/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;46,211,243,281,442/Binding site: carbohydrate predicted
F;216,454/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
F;216,454/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
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A; Molecule type: mRNA
A; Residues: 1-25; 'N', 227-257, 'S', 259-367, 'K', 369-455 < AUF>
A; Residues: 1-225; 'N', 227-257, 'S', 259-367, 'K', 369-455 < AUF>
R; Kehry, M.; Sibbey, C.; Fuhrman, J.; Schilling, J.; Hood, L.E.
R; Kehry, M. A: Sci. U.S.A. 76, 2932-2936, 1979
A; Reference number: A2624; MUID:79223904; PMID:111247
A; Contents: annotation; MOPC 104E
A; Note: this sequence has been revised in reference A02039. Carbohydrate binding sites
A; Note: this sequence has been revised in reference A02039. Carbohydrate binding sites
A; Note: this sequence has been revised in reference A02039. C.H.; Hood, L.E.
Biochemistry 21, 5415-5424, 1982.
Biochemistry 21, 5415-5424, 1982.
A; Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain
A; Reference number: A02039; MUID:83075344; PMID:6816276
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R;Auffray, C.;
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
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A; Residues: 1-77,'N',79-100,'Q',102-225,'N',227-257,'T',259-367,'K',369-455 <KEH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: the
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Best Local
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                                              PSRDELT-KNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD--SDGSFFLY
                                                                                                                                                                             STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE-----PQVYTLP
                                                                                                                                                                                                                                    --Trtippsfad-iflsksanltclvsnlatye-tlniswasosgepletkikimeshpn
                                                                                                                                                                                                                                                                                                                                                                                                        ----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGG
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                                                                                                                  GTFSAKGVASVCVEDWNNRKEFVCTVTHRDLPSPQKKFISK----PNEVHKHPPAVYLLP
                                                                                                                                                                                                                                                                                               PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                          YKVISTLTISEIDWLNLNVYTCRV--DHRGLTFLKNVSSTCAASPST-----DIL--
PAREQLNLRESATVTCLVKGFSPADISVQWLQRGQLLPQEKYVTSAPMPEPGAPGFYFTH
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A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
EMBO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog A;Reference number: A23195; MUID:84207910; PMID:6327276
A;Accession: A23195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; R;Flanagan, J.G.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant A;Reference number: A22771; MUID:84236029; PMID:6234164
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Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon
A;Reference number: 136948; MUID:87147196; PMID:3103123
A;Accession: 136948
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A; Residues: 1-428 < FLA>
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A; Residues: 1-426 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                      Ig epsilon chain C region - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT-QKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPREPQVYTL-----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN--SDTHLLQGQSLTLTLESPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----STASATQEGELASTQSELTLSQXHWLSDRTYTCQVTYQGGTFE------
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Pred. No. 2.6e-14;
4; Mismatches 136;
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k; Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: A53116
A;Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167 A;Experimental source: B cell myeloma U-266 A;Note: sequence extracted from NCBI backbone (NCBIP:125297)
                                                                                                                                                                     Eur. J. Immunol. 23, 159-167, 1993
A;Title: Characterization of four novel epsilon chain mRNA and a A;Reference number: A46536; MUID:93122085; PMID:8419166
A;Accession: C46536
                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-358,'L',360-428 <MAX>
A;Cross-references: GB:U00222; NID:g184755
A;Cross-references: GB:U00222; NID:g184755
A;Note: this sequence difference may be due to polymorphism
R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments,
A;Reference number: A94418
A;Accession: A94418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A;Title: Purification and characterization
A;Reference number: S02438; MUID:88083554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 1-40;68-114;427-428 <KEN>
A;Cross-references: GB:L00022; NID:gl
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A;Title: Cloning and sequence determination of the gene A;Reference number: A93933; MUID:83065234; PMID:6815656
A;Accession: B93933
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A;Title: Duplication and deletion in the human immunoglobulin epsilon
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A;Cross-references: EMBL:X63693; GB:S38668; NID:g32987
A;Cross-references: T.; Ono, Y.; Onda, H.; Sasada, R.;
Nucleic Acids Res. 11, 719-726, 1983
A;Title: Molecular cloming and nucleotide sequencing of
A;Reference number: A93491; MUID:83168897; PMID:6300763
A;Accession: A93491
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J. Exp. Med. 176, 233-243, 1992
A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing A;Reference number: PHI214; MUID:92308839; PMID:1613458
A;Accession: PHI214
                                                                                          A; Molecule type: mRNA
A; Residues: 382-426 <HEL>
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A;Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L'
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ell 29, 691-699, 1982
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;Residues: 1-428 <SEN>
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                                                                                                                                             compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a recombinant human IgE Fc-epsilon PMID:3121387
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                                                EMBO J. 7, 739-744, 1988
A;Title: Chicken immunoglobulin gamma-heavy chains: limited
                                                                                    C;Accession: S00390
R;Parvari, R.; Avivi, A.; Lentner,
EMBO J. 7, 739-744, 1988
A;Reference number: S00390; MUID:88283642; PMID:3135182 A;Accession: S00390
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A;Cross-references: GDB:119335; OMIM:147180
A;A;Map position: 1432.33-1432.33
A;A;Map position: 1432.33-1432.33
A;Introns: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap: nain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la: C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin homology <IM1>
F;22-87/Domain: immunoglobulin homology <IM1>
F;22-195/Domain: immunoglobulin homology <IM2>
F;332-301/Domain: immunoglobulin homology <IM3>
F;338-407/Domain: immunoglobulin homology <IM4>
F;338-407/Domain: immunoglobulin homology <IM4>
F;14-10isulfide bonds: interchain (to light chain) #status predicted
F;11,49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;121,209/Disulfide bonds: interchain (to heavy chain) #status predicted
Ig gamma chain (clone 36) - chicken (fr
N;Alternate names: Ig nu chain
C;Species: Gallus gallus (chicken)
C;Date: 07-Sep-1990 #sequence_revision
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A; Residues: 382-391 (ABD2)
A; Cross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1;
A; Experimental source: B cell myeloma U-266
A; Note: sequence extracted from NCBI backbone (NCBIP:125299)
A; Accession: A46536
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A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIP:123483)
                                                                                                                   S00390
                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSCDKTHTCPEL-LGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEP 207
                                                                                                                                                                                                                         QPRKTKGSGFFVFSRLEVTRAEWEQKDEFI CRAVHEAASPSQTVQRAVSVNPG
                                                                                                                                                                                                                                                                          PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT-QKSLSLSPG
                                                                                                                                                                                                                                                                                                                                 PRAAPEVYAFATPEWPGSRDKRT
                                                                                                                                                                                                                                                                                                                                                                                QPREPQVYTL-----PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN--GQPENNYKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DSTKKCADSNPRGVSAYLSRPSPFD-LFIRKSPTITCLVVDLAPSKGTVNLTWSRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----STASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFE----
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                                                                                     (fragment)
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     07-Sep-1990 #text_change 11-Jan-2000
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F;130-202/Domain: immunoglobulin homology <IRM2>
F;242-310/Domain: immunoglobulin homology <IRM2>
F;242-310/Domain: immunoglobulin homology <IRM3>
F;349-420/Domain: immunoglobulin homology <IRM3>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;28-90,137-200,249-308,356-419/Disulfide bonds: #status predicted
F;46,114,212,261,277,284,445/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;219,457/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
F;296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; prize splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; prize splicing; cIMMI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig mu chain C region, secreted form - rabbit C;Species: Oryccolagus cuniculus (domestic rabbit) C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change
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A;Cross-references: EMBL:X07174
A;NOTC: this sequence was determined from the differentiated gene C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: immunoglobulin
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R;Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.
J. Immunol. 132, 490-495, 1984
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      NDRADSRRSLWDQGNFPLIIKNLK--
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                                                                                                          AATQGNKVVLGKKGDTVELTCTASQ--KKSIQFHW--KNSNQIKILGNQGSFLTKGPSKL
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Pred. No. 3.4e-14;
                                                                                                                                               Score 360; DB 1;
Pred. No. 3.5e-14;
6; Mismatches 145
                                                                     CLARDFLPSSVTFSWSFKNNSEI --
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    -IEDSDTY-ICEVEDQKEEVQLL
                                                                                                                                                                                        Length 458;
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                                                                                                                                                                     RESULT 73
S03961
                                                                                                 Ig mu chain C region - house shrew (fragment) C;Species: Suncus murinus (house shrew) C;Date: 28-Feb-1990 #sequence_revision 28-Feb
A;Title: Nucleotide sequence of Suncus murinus immunoglobulin A;Reference number: S03961; MUID:89232144; PMID:2497033
                                           C;Accession: S03961
R;Ishiguro, H.; Ichihara, Y.; Namikawa, FEBS Lett. 247, 317-322, 1989
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A; Introns: 17/1
C; Superfamily: 7
                                                                                                                                                                                                                                                                                 A;Cross-references: GB:S79267; NID:g1086922; PIDN:AAB35273.1; PID:g1086923
                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-71 < RES>
                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                               Vopr. Virusol. 40, 100-102, 1995
A;Title: [Nucleotide sequence of two exons
A;Reference number: I60082; MUID:95407135;
A;Accession: I60082
                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: I60082
R;Zverev, V.V.; Sidorov, A.V.; Nedospasov, S.A.; Maliushova, V.V.; Udalova, I.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4 receptor - human (fragment)
                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Species: Homo sapiens (man)
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                                                                                                                                                                      Similarity
                 ILGNOGSFLTK 71
                                                                                               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                       MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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ILGNQGSFLTK
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                                                                                                                                                                                                                          T-cell surface glycoprotein CD4; immunoglobulin
                                                                                                                                                  Conservative
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98.6%;
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                                                                                                                                                                    Score 357;
Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                               of the human
PMID:7676667
                                                                                                                                                                    DB 2;
5.7e-15;
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28-Feb-1990

#text_change 21-Jan-2000

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A;Experimental source: spleen C;Genetics:
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 21-Jan-2000
C:Accession: S25644
                    ş
                                                                                                                                A;Map position: 6
C;Superfamily: immunoglobulin C region; immunoglobulin C;Superfamils: immunoglobulin C;Keywords: immunoglobulin F;234-305/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                              R;Parker, K.; Bugeon, L.; Soulillou, J.P. submitted to the EMBL Data Library, September 1992
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A; Residues: 1-343 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S03961
A;Molecule type: DNA
A;Residues: 1-457 <ISH5
A;Cross-references: EMBL:X13920
                                                                                                                                                                                                                                                                                              A;Accession: S25644
                                                                                                                                                                                                                                                                                                             A; Reference number: S25644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Superfamily: immunoglobulin C
Keywords: immunoglobulin
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Best Local
                                                          Matches
                                                                                          Query Match
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Matches 122;
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                                                        87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYVTSNPTPEPQNPGLYFVHSILTVSEKDWSSGESFSCVVGHEALPLSVTEKAVDKTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QSLSRPKDVANDPPSVFVLPPAQEQLKLRESASITCLVKDFSPPDVFVQWQHHGQPVDPK 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALHKGLTFQKNVSSVCMGDDTSTGISVFLLPPTFAN-IFLTQSAQLTCLVTGLATYD-SL
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                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                            immunoglobulin homology <IMM>
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                                                                       13.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LG-----GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -ELQVTPELPPNVSIFV---PPR--NSFSGNHPRTSQLICQASGF
                                                      66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region; immunoglobulin
                                                                       Score 353; DB 2;
Pred. No. 6.4e-14;
                                                                                                                                                                                                                                     NID:g56461;
                                                        Mismatches 107;
                                                                                                                                                                                                                                     PIDN:CAA48392.1; PID:g818025
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                                                                                      Length 343
                                                        Indels
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                                                      30;
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                                                      Gaps
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F;238-306/Domain: immunoglobulin homology <IMM3>
F;338-306/Domain: immunoglobulin homology <IMM3>
F;345-416/Domain: immunoglobulin homology <IMM4>
F;345-416/Domain: immunoglobulin homology <IMM4>
F;45,112,139,192,210,238,257,280,326,441/Binding site: carbohydrate (Asn)
F;135-198,245-304,352-414/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lighand disulfide bonds. In some cases, such as IQA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-90/Domain: immunoglobulin homology <IMM1>
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A;Note: the sequence was determined from A;Note: the authors translated the codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 13, 5611-5628, 1985
A;Title: Phylogenetic conservation of immunoglobulin heavy
A;Reference number: A02168; MUID:85297761; PMID:2994005
A;Accession: A02168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McGuire, K.L.; Duncan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: 30-Jun-1987 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Species: Mesocricetus auratus (golden hamster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mu chain C region - golden hamster
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EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR-EPQVYTLP
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                                                                    ----DIQAFPIPPSFVGIFLNKSATLTCLVTNLATYD-TLNISWSSRSGEPLETKTKLTE
                                                                                                                                                                                                                                            SVFVPSRDAFSGPAPRKSRLFCEASNFSPKQITVSWLRDGKPVKSGFTTEPVTPEDRGSG
                                                                                                                                                        PRTYKVISTLTITESDWLNLSVYTCRV--DHRGLTFWKNVSSTCAASPST------
                                                                                                                                                                                                                                                                                                                                  P---PKSVLEGSDEYLVCKVHHGNTNKDLRVPIPGVT
                                                                                                                                                                                                                                                                                                                                                                           PLIIKNLKIEDSDTY-ICEVE--DQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGS 149
                                                                                                                                                                                                                                                                                                                                                                                                                        VAMGCLARDFLPSSISFSWNYQNKSEV--NQGVRTFPTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELTCTASO -- KKSIOFHWKNSNOIKILGNOG -- SFLTKGPSKLNDRADSRRSLWDQGNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPGAPGLYFTHSILTVTEEEWNSGETYTCVVGHEALPHMVTERTVDKSTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNTKIMESHPNGTFSAVGVASVCMEDWDNRKEFVCTVTHRDLPSPQKKFISK----PNEV
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                                                                                                          LGGPSVFLFPPKPKDT-LMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                                 -----KTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PQVYTLPPSRDEL-TKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPVL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 349; DB 1;
Pred. No. 1.6e-13;
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for residues 105 and 324 as Val
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                                                                                                                                                                                                                                                                                       -GKNIQGG----
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Ig gamma-2a chain C region (E5.7A12) - mouse (fragm C;Speciles: Mus musculus (house mouse) C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 C;Accession: B30503 R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K. J. Immunol. 141, 1754-1761, 1988 A;Title: DNA rearrangements affecting both variable
                                                                                                                            RESULT
B30503
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Proc. Natl. Acad. Sci. U.S.A. 85, 2245-2249, 1988
A;Title: Amino acid sequence of heavy chain from Xenopus
A;Reference number: A94192; MUID:88178921; PMID:2451244
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A; Residues: 1-453 < SCH>
C; Superfamily: immunoglobu.
C; Keywords: immunoglobu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig mu chain C region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Datc: 31-Mar-1990 #sequence_revision 30-Jun-1992 #text_change
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Best Local S
Matches 119
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 rearrangements affecting both variable
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                                                                                                                                                                                                                                                                                                                                                                               LHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTLYSCVV-----EHAESGSLQEKNMSKSLMCDTPITPTSIQVITIPPS-LESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VCLATNFTPTHI-----VIKWLKNGNQTTEGVRVEEPVEDKKRGYEATSYLSITRKEWDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVWD--NIEQFYCNAKHLDT---IKSVELKKDPVKPVEKPVVSIHPPSKDALALNESLFI
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                                                                                                                                                                                                                                    GNVFSCSVMHEALHNHYTQKSLSLSPG-----LQLDETC
                                                                                                                                                                                                                                                                                                                                             CADEWNNOK-FVCKVEHTELASMKEVFLFKEKGEYNTPSVYVFPPPLEELSKRETATLTC
                                                                                                                                                                                                                                                                                                                                                                                                                  FEKKSATLTCLVSNMANSEDLRSISWFKKSGTQEIPLKTELGDAIYNDNRTYSVKGTTTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTCPELLGGPS--VFLFPPKPKDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGLTAN-SDTHLLQGQSLTLTLESPPGSSPSVQCRSP---RGKNIQGGKTLSVSQLELQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQ-----
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                                                                                                                                                                                                                                                                       LVKGFSPSEIFVKWLHKNEAVPKQNYINTSINDELLPKGQKSGKFFLYSLHTIDIKDWDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISRTPEVTCVVVDVSHEDPEVKFNWY-VDGVEVHNAKTKPREEQYNS--TYRVVSVLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHPNGTFSAIGEANVCVEDWDSGKEFVCTVTHRDLPSPQKKFISKPRGMNKTPPAVYQQP
                                                                                                                                                                                                GDSFSCVVGHESLPLQLTQRSIDKSSGKPTNVNVSLVLSDTC
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25.8%; Pre-
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Pred. No. 2.5e-13;
77; Mismatches 189;
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                                                                      #text_change
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A;Reference number: A30503; MUID A;Accession: B30503 A;Molecule type: mRNA A;Residues: 1-112 <GIL> A;Cross-references: GB:M21925 A;Experimental source: myeloma c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Vazquez, M.; Mizuki, N.; Flajnik, M.F.; McKinney, E.C.; Kas
Mol. Immunol. 29, 1157-1158, 1992
A; Title: Nucleotide sequence of a nurse shark immunoglobulin
A; Reference number: I50731; MUID:92357056; PMID:1495502
A; Accession: I50731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1g neavy chain - nurse shark
C;Species: Ginglymostoma cirratum (nurse shark)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50731
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C;Superfamily: immunoglobulin C region; immunoglobulin
F;469-539/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues:
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                                                                                                                                                                                           PGQGLEWIVYYYSSSMNNYAPAIKDRFTAAK---DTSNNIFALEMRSVKIDDTAIYYC--
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CEVRHSGSDKSTGMPCPDGFPTALLTVSSSEEIESRKFAIIVCSISDFHSKSISVTW---
                                                                                                                            ----TRRMSGYEYLGGHSGYWGQGTMVTVTTATP--SSPTLYGLVSSCQQGNIDGSVIY
                                                                                                                                                             EDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV-----QCRS-----
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                                 -ELODSG-
                                                               GCLAMDYSPDVASVTWKKHGQLITTGVQTYPSVRNKKGTYTLS-SQLALIESDAECDQIS
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ilarity 50.0%;
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the codon GAG f
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Pred. No. 5.1e-
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Pred. No. 3.2e-13;
7; Mismatches 22
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                                                                                                -----PRGKNIQGGKTLSVSQL-----
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A; Cross-references: EMBL: X69492; NID: g62420; PID: g62421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig upsilon chain - axolotl (fragment)
C;Species: Ambystoma mexicanum (axolotl)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
C;Accession: S31436
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                      LDSD----
                                                                                      GQPREPQVYTLPPSRDELTK-NQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPV 382
                                                                                                                           EGPEEAAVISEQYIDSDGTFTAMSYLNITKNEWERGDEFTCKVKHFDLPFPLSRSVSKPT
                                                                                                                                                               TKPRE-----EQY---NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 325
                                                                                                                                                                                                CADSQTPYQPKVFLIAPKARD-LYIANQPVVICKITKMENSD-SLSVTW-----KRR 259
                                                                                                                                                                                                                                     CPELLG--GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                                                                                                                                                        QKDGQGTFSTTSQINVTKSDWASGDKYTC-----KVEH-----PATSSRAEDTIHN
                                                                                                                                                                                                                                                                                                       GKNIQG----GKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHT
                                                                                                                                                                                                                                                                                                                                            DTDGNGSIELVCLISGYTPDNIQVRWLVNDKMAPIQGQT--
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                                                       GRSFAPTMYVFAPHEMELANYDFVSLTCLVKSFSPDDIYIQWKQGKSVIPSDKYVSMEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYI-----CEVEDQKEEVQL-----
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GSFFLYSKLTVDKSRWQQGNVFSCSVMHEAL 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.9%;
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Pred. No. 6.3e-12;
5; Mismatches 146;
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RESULT 80
A39016
T-cell surface glycoprotein CD7 precursor -
T-cell surface rames: T-cell leukemia antigen
A;Molecule type: mRNA
A;Residues: 1-438 <KOK>
A;Cross-references: EMBL:X07784; NID:g63963;
A;Note: the sequence was determined from the
                                                                                                                                                                                       C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999 (;Accession: S00980 R;Kokubu, F; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W. EMBO J. 7, 1979-1988, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A39016; S03520

R;Schanberg, L.E.; Fleenor, D.E.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
Proc. Natl. Acad. Sci. U.S.A. 88, 603-607, 1991

A;Title: Isolation and characterization of the genomic human CD7 gene: structural simila A;Reference number: A39016; MUID:91110576; PMID:1703303

A;Accession: A39016
                                                                                                                  A; Reference number: S00980; A; Accession: S00980
                                                                                                                                         A; Title: Complete structure and organization of immunoglobulin heavy A; Reference number: S00980; MUID:88328985; PMID:3138109
                                                                                                                                                                                                                                                                                             Ig mu chain C region (clone 12022) - horn shark (fragment)
C;Species: Heterodontus francisci (horn shark)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GDB:119770;
A; Map position: 17q25.2-17q25.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Aruffo, A.; Seed, B.
EMBO J. 6, 3313-3316, 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-240 <ARU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M37271; NID:g180163; PIDN:AAA51953.1;
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;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPDPPAASALPAALAVISFLLGLGLGVACVLARTR 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN--VFSCSVMHEALH 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LALARGLPGALAAQEVQQSPHCTTVPVGA-----SVNITCSTSGGLRGIYLRQLGPQPQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NVYGSGTLVLVTEEQSQGWHRCSDA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DI-IYYEDGVVPTTDRRFRGRI-DFSGS---QDNLTITMHRLQLSDTGTYTCQAITEV--
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Pred. No. 6.2e-12;
3; Mismatches 54;
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PIDN:CAA30617.1; PID:g63964 differentiated gene

regio

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C;Species: Lepisosteus osseus
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change
C;Accession: I50830
R;Wilson, M.R.; van Ravenstein, E.; Miller, N.W.; Clem, L.W.;
Dev. Comp. Immunol. 19, 153-164, 1995
A;Title: cDNA sequences and organization of IgM heavy chain ge
A;Reference number: I50006; MUID:96039719; PMID:7556802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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F;228-291/Domain: immunoglobulin homology <IM3>
F;330-400/Domain: immunoglobulin homology <IM4>
F;330-400/Domain: immunoglobulin homology <IM4>
F;166,200,245,275,374,411,415,425/Binding site: carbohydrate (Asn)
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                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-474 <WIL>
A; Cross-references: EMB
C; Genetics:
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                                                              Query Match
Best Local S
Matches 116
                                                                                                                                                                                                                                                                                                                                                                                                      g mu chain - Lepisosteus osseus (fragment)
;Species: Lepisosteus osseus
;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 03-Nov-2000
                                                                                                                                              Superfamily:
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                                                                                   Similarity
GKKGDTVELTCTAS--QKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTCLVKGFYPSDIAVEWESNGQPEN--NYKTTPPVLDSDG-SFFLYSKLTVDKSRWQQGN
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                                                                                                                                         immunoglobulin C region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                Conservative
                                                                                                                                                                                                      EMBL: U12455; NID: g529949; PIDN: AAC59688.1; PID: g529950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.5%; Score 312; DB 1; 25.4%; Pred. No. 2.3e-11;
                                                                                 11.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                              Score 308.5; DB 2
Pred. No. 4.2e-11;
2; Mismatches 171
                                                                                                                                                                                                                                                                 from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419
                                                                                                                                            immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431
                                                                                                    DB 2;
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                                                                                                                                            homology
                                                                Indels
                                                                                                  Length
                                                                                                                                                                                                                                                                                                                           genes in two holostean fish
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T-cell surface glycoprotein CD4 (allele 1) - pig (f C;Species: Sus scrofa domestica (domestic pig) C;Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 C;Accession: 147131; S21461 R;Gustafsson, K.; Germana, S.; Sundt, T.M. J. Immunol. 151, 1365-1370, 1993 A;Title: Extensive allelic polymorphism in the CDR2 A;Reference number: 147131 MUID:93329116; PMID:833 A;Accession: 147131
                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-99 < GU2>
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                                                                                                                                 Query Match
Best Local S
Matches 59
                                                                                                                                                                                                                  ;Superfamily: T-cell surface glycoprotein CD4; ;Keywords: glycoprotein; T-cell
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                                                                                                                                                   Local Similarity
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                 NFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTAN
                                                                                  KKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFL-TKGPSKLNDRADSRRSLWDQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLDEGVTNIPATVDĖKKLYSASSLLTVTEKDWKSSAEFAČEFVHKTGSVLKNITYTSREČ
                                                                  KAGDLAELPCHSSQKKNLPFNWKNSNQTKILGGHGSFWHTASVTELTSRLDSKKNMWDHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSVYSKYTISSSDWNSGTMYSCAVHHETAPLPVSVITRTTDSSTGKATLVNFTLNLPDTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFLYSKLTVDKSRWQQGNVFSCSVMHEA-----LHNHYTQKSLSLSPGLQLDETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VYTLPPSRDE--LTKNQVSLTCLVKGFYPSDIAVEW--ESNGQPENNYKTTPPVLDSDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAPEFGHEGGKIVAVSRVSVVLEKWRTGTEYKCIVSHLDSFPTPITKTYKRQIATKIRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN-KALPAPIEKTISKAKGQPREPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QETV---KVVIEPPTNEEQ-FVKKTATLTCRRIALVSTS----DVSMTWSSGGKPL--AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELLGGPSVFLFPPKPKDTLMISRTPEVTC---VVVDVSHEDPEVKFNWYVDGVEVHNAK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TPPVPPASVLLNPP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTSGDVVALGCLATGFLPDSLTFKWTDSTDKEL----TPFRKYPSVLNGETYSSTS---
SFPLIIKNLEVTDSGIYICEVEDKRIEVQLLVFRLTAS
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                                                                                                                                                                                                  immunoglobulin homology <IMM>
                                                                                                                                     Conservative
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                                                                                                                                                 11.3%; Score 305.5; DB 2 60.2%; Pred. No. 9.7e-12;
                                                                                                                                   16;
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                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                       the CDR2-like PMID:8335933
                                                                                                                                                                                                                                                     PIDN:CAA46583.1;
                                                                                                                                                                                                                                   immunoglobulin
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BWine

Ig mu chain C region, membrane-bound (clone 3050) - horn shark C;Species: Heterodontus francisci (horn shark) C;Date: 30-Jun-1991 #sequence revision 30-Jun-1991 #text_change C;Accession: S01854; C32716; Ā46530 R;Kokubu, F; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, GEMBO J. 7, 1979-1988, 1988 EMBO J. 7, 1979-1988, 1988 A;Reference number: S00980; MUID:88328985; PMID:3138109

#text_change

16-Aug-1996

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chain

constant

HVRKCO

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Ig alpha chain - chicken
C;Species: Gallus gallus (chicken)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C;Accession: A46507
R;Mansikka, A.
J. Immunol. 149, 855-861, 1992
A;Title: Chicken IgA H chains. Implications concerning the evolution of u of
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A46507
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F;228-291/Domain: immunoglobulin homology <IMM3>
F;330-400/Domain: immunoglobulin homology <IMM4>
F;330-400/Domain: immunoglobulin homology <IMM4>
F;438-458/Domain: transmembrane #status predicted <TMM>
F;27-85,130-188,235-289,337-398/Disulfide bonds: #status predicted F;27-85,275,374,411,415,437/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobuf;20-87/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: the sequence was determined from the germline gene R;Kokubu, F.; Hinds, K.; Litman, R.; Shamblott, M.J.; Litman, G.W. Proc. Natl. Acad. Sci. U.S.A. 84, 5868-5872, 1987
A;Title: Extensive families of constant region genes in a phylogenetically primitive A;Reference number: A32716; MUID:87289703; PMID:3475706
A;Accession: C32716
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A; Residues: 1-99 < KO2>
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nes 121; Conserv
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                                                                                                                                                                                                                                                                                                                              DKSVNPGNYKNTEVMAENDNSSYFIYSLLSIAAEEWASGASYSCVVGHEAI-----
                                                                                                                                                                                                                                                                                                                                                                       GOPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN 369
                                                                                                                                                                                                                                                                                                                                                                                                                      DLPTPLRASIHKEEVKDLREPSVSILLSPAEDVSAQRFLSLTCLVRGFFPREIFVKWTVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDGQHMESGFVTSPT--C----GVNGTFSATSRLTVPAREWFTNKVYTCQV--SHQGVTQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF 195
                                                                                                                                                                                                                                           ---PLKIINRTVNKSSDSS-DHIWIEDNEEESAI
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Nature 374, 168-173, 1995
A;Title: A new antigen receptor gene family that undergoes
A;Reference number: S60266; MUID:95183140; PMID:7877689
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S60266
R;Greenberg, A.S.; Avila, D.; Hughes, M.; Hughes,
Nature 374, 168-173, 1995
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A;Accession: A46507
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-585 <MAN>
A;Residues: 1-585 <MAN>
A;Cross-references: GB:S40610; NID:g251907; PID:g251908
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:109906, NCB
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic A;Molecule type: mRNA A;Residues: 1-684 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel antigen receptor precursor - nurse shark
C;Species: Ginglymostoma cirratum (nurse shark)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change
                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U18701; NID:g699442; PIDN:AAB48195.1; PID:g699443
                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S60266
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                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKNAG 566
                                                     VEYTCSAKQDQSSTPVVKRTRKARVEPTKPHLRLLPPSPEEIQSTSSATLTCLIRGFYPD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPAATOGNKVVLGKKGDTVELTCTASOKKSIOFHWKNSNOIKILGNOGSFLTKGPSKLND
IIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQ 154
                                                                                                       VELTCTASQKKSIQFHWKNSNQIKILGNQG--SFLTKGPSKLNDRADSRRSLWDQGNFPL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOPISPONYLIFGP--EKDGDFYSLYSKLKVSVEDWQRGDVFGCVVGHDGIPLNFIHKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQP--ENNYKTTPPVLDSDGSFF-LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GV-VVAEESIRKETDTPLHAPSVYVFPPPAEELSLQETATLTCMASSFLPSSILLTWTQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPAPIEKTISKAKGQP-REPQVYTLPPSRDELT-KNQVSLTCLVKGFYPSDIAVEWESN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-GVSVSWSRSSGGGLDV----SQTEDRQADGRYTVRSFLRVCAEEWNGGETFGCSVREE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPEVKFNWYVD---GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNEEMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ADVKETIGGDGVCPIFTSKVTLLSDPTQ----EDFERRVLLVCLVEGLPSAGAAIQWLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL--LVFGL-TANSDTHLLQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPVATTGGTYSL----TTALTVPREQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----EPVTATVSTDCDAT---PQL----QVSLLPPTLEE-LLVSHNATVTCVVSNAAAA 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FKIDIVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVE 194
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- PAPESDESGCSDCTESGVTQWSRVNVTRKSWEGGAQFGCRVTHGALK--
                                                                                                                                                                                     11.2%;
                                                                                                                                                                                                                                                                                                                                                       acid sequence
                                                                                                                                                            ; Score 301.5; DB 2; pred. No. 1.7e-10; 66; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                       not
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                                                                                                                                                                                                              Length 684;
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Mol. Immunol. 31, 633-642, 1994

A;Title: Characterization of a C alpha gene of swine.

A;Reference number: I47175; MUID:94254897; PMID:7545929

A;Accession: I47175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig alpha chain C region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change
C;Accession: I47175
R;Brown, W.R.; Butler, J.E.
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C;Superfamily: im
F;232-304/Domain:
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
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Best Local (
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                                                                                                                                                                                                   219
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SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG----LQLDETCAEAQ 442
                                 PSEELALNELVTLTCLVRGFSPKDVLVRWLQGGQELPRDKYLVWESLPEPGQAIPTYAVT
                                                                  SRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNY---KTTPPVLDSDGSFFLY
                                                                                                 DSC-GCYSVSSILPGCADPWNKGETFSCTAAHSELKSALTATITKPKVNTFRPQVHLLPP
                                                                                                                                                                  CC-KPSLSLQPPALAD-LLLGSNASLTCTLSGLKKSE-GVSFTWQPSGGK-DAVQASPTR
                                                                                                                                                                                                   LLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE
                                                                                                                                                                                                                                                                      QDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTH--
                                                                                                                                                                                                                                                                                                     LTLGSSEPAGYVVIACLVRDFFPSEPLTVTWSPSREGVIVRNFPPAQAGGLYTMSSQLTL
                                                                                                                                                                                                                                                                                                                                    LTLTLESPPG------SSPSVQCRSPRGKNI------QGGKTLSVSQLEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALH-----NHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-VKFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRSPRGKNIQGGKTLSVSQLELQDSGTWTCT------
                                                                                                                               EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                    ------PVEQCPADQILKCQVQHLSKSSQSVNVPCKVLPSDPCPQ
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27.1%;
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                                                                                                                                                                                                                                                                                                                                                                                       Score 300; DB 2;
Pred. No. 9e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from
                                                                                                                                                                                                                                                                                                                                                                      Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                       Length 342;
                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                      -----TCPE
                                                                                                                                                                                                                                                                                                                                                                       76;
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RESULT 88
S09264
                                                            Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin C region; immunoglobulin C;Keywords: immunoglobulin F;124-190/Domain: immunoglobulin homology <IMM>
                                                                                                                            A; Molecule type: DNA
A; Residues: 1-357 < BUR>
                                                                                                                                                                                    A; Accession: S09269
                                                                                                                                                                                                      A; Title: The IgA heavy-chain gene family in rabbit: cloning A; Reference number: S09264; MUID:90076124; PMID:2512120
                                                                                                                                                                                                                                           R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
                                                                                                                                                                                                                                                                                C; Accession: S09269
                                                                                                                                                                                                                                                                                                                                                          S09269
                                                                                                                                                                                                                                                                                                                                                                           RESULT 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-339 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120 A;Accession: S09264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan.1993 #sequence_revision 29-Jan-1993
C;Accession: S09264
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                                                                                                                                                                   A;Status: not compared with
                                                                                   Superfamily: immunoglobulin C region; immunoglobulin; Keywords: immunoglobulin
                                    Query Match
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Matches
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                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 LTLESPPGSSPSVQCRSPRGKNIQG------
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 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALVTLTCLVRGFSPKDVLVYWTNKGVVVPKDSFLVWKPLPEPGQEPTTYAVTSLLRVSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVLPGCAETWIAGTEFICTVIHPEIEGSSLIATIRKDIGSLIPPQVHLLPPPSEELALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LONOKKVEF-----KID---IVPCPAPEPKSCDKTHTCPEL-LGGPSVFLFPPK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DWNQGDSYSCVVGHEGLAEHFTQKTIDRQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSVLTVLHQDWLNGKEYKCKVSNKALP-APIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKDTLMISRTPEVTCVVVDVSHEDP-EVKFNWYVDGVEVHNAKTKPREEQYN---STYRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSLPCPLSGQPVVV-----GCLIQGFFPLGPLNVKWTISGENVTFPPVQLDTSGLYTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRD-LLLGSDASLTCTLRGL--KDPKDAVFTW----EPTNGNEPVQQSPQRDPCGCYSV
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 Conservative
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                                                                       immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.0%;
11.0%; Score 296; DB 2;
29.8%; Pred. No. 1.6e-10;
tive 40; Mismatches 104
                                                                                                                                                               conceptual
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                                                                                                                                                                   translation
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                                    Length 357;
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Indels
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68;
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into c;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;49-133/Domain: immunoglobulin homology <IMM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Dahan, A.; Reynaud, C.A.; Weill, J.C.
Nucleic Acids Res. 11, 5381-5389, 1983
A;Title: Nucleotide sequence of the constant region of a A;Reference number: A02170; MUID:83299221; PMID:6310496
A;Accession: A02170
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MHCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;151-219/Domain: immunoglobulin homology <IMM3>F;258-329/Domain: immunoglobulin homology <IMM4>F;347-367/Domain: carboxyl-terminal <CTS>
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-367 < DAH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g mu chain C region - chicken (fragment)
;Species: Gallus gallus (chicken)
;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Accession: A02170
                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                          VFPPPTEQLNGNQRLSVTCMAQGFNPPHLFVRWMRNGEPLPQSQSVTSAPMAENPENESY
                                                                                 TLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDS--DGSF
                                                                                                                            -RVLQSNGLYTVDGVATVCASEWDGGDGYVCKVNHPDLLFPMEEKMRKTKASNARPPSVY
                                                                                                                                                                                                                                                                                                                                          GKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVPCPAPEPKSCDKTHTC---
FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                   PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK-GQPREPQVY
                                                                                                                                                                                                              PVVQQDIAIRVITPSFVD-IFISKSATLTCRVSNMVNADGLEVSW-WKEKGGKLETALGK
                                                                                                                                                                                                                                                     PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP-EVKFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                    GPEVVAESRISVTESEWDTGATFSCVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS 429
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                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    48; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 296; DB 1;
Pred. No. 1.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 367;
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R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09272
A;Status: not compared with conceptual translation
                                                                                                                                                                                Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan.1993 #sequence_revision 29-Jan.1993
C;Accession: S09272
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A;Title: Evolution of vertebrate IgM: complete amino acid sequence of the constant region A;Reference number: A46532; MUID:93011455; PMID:1382992
A;Accession: A46532
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A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: nucleic acid
A; Residues: 1-454 <FEL>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQKPNGNQRRKPSVYIYPPPSEELALKETATIVCLMRGYHPCDLFVRWLENSQQLQKQDY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKDVTSG--IYTEEPVADTAGNFDVTSLLNIEPMDWNMDTVYSCVVDQTASKFWNTRNMS 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPSLGQPLTKKVQFSVQRISKPTVTLHAPAREDIINNNATIVCICRGFHPQPISIKWMKN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLYSASTRVKVPSESW-------KORDPYYCKV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATQGNKVV----LGKKGDTVELTCTAS--QKKSIQFHWKNSNQIKI----LGNQGSFLTK 71
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23.1%;
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Pred. No. 2.2e-10;
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                                                                                                       sequence analysis of 13
                                                                                                                                                                                                                  16-Jul-1999
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A;Residues: 1-343 <BUR>
C;Superfamily: immunoglo
C;Keywords: immunoglobul
F;232-305/Domain: immuno
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A;Map position: 14q32.33-14q32.33
A;Introns: 1/1 103/1; 210/1
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R;Flanagan, J.G.; Lefranc, M.P.; Rabbitts, Cell 36, 681-688, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig alpha-2 chain C region (allotype A2m(1)) - human
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Jul-1999
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A; Residues: 1-340 < FLA>
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Matches 103
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;230-302/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                Superfamily: immunoglobulin C region; immunoglobulin
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                                                                                                                                                                                                                    122 VFGLTANSDTH------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNIQGGKT
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                                                                                                             TTSSQLTLPATQCPDGKSVTCHVKHYTNPSQ---DVTVPCPVPPPPPC-----C----H 111
                                                                                                                                             LSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG
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STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                  PRLSLHRPALED-LLLGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPPERDLC 167
                                                                      PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                  VFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDASGDLY
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                                                                                                                                                                                                                                                                        10.9%; Score 294.5; DB 2; 29.2%; Pred. No. 1.9e-10;
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                                                                                                                                                                                                                                                     50; Mismatches 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-438 <KOK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
SLSPG
                                    DKSVNPGNYKNTEVMAENDNSSYFIYSLLSIAAEEWASGASYSCVVGHEAIPLKIINRTV
                                                                                                                                ALPAPIEKTISKAKGQP-REPQV-YTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN
                                                                                                                                                                                                                                                                                             KIDI----VPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 251
                                                                                                           DLPTPLRASIHKEEVKDLREPSVSILLSPAEDVSAQRFLSLTCLVRGFFPREIFVKWTVN
                                                                                                                                                                                                                                                       SRNITGSQVPC-----SCN------DPVIKILPPSIEQVL-LEATVTLTCV---V
                                                                      GQPEN--NYKTTPPVLDSD-GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL 426
                                                                                                                                                                                  SNAPYGVNVSW----TQEQKSLKSEIAVQPGEDADSVISTVNISTQAWLSGAEFYCVVNHQ
                                                                                                                                                                                                                    SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 311
431
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414

354 369 294

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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplicationn; glycoprotein; heterotetramer; immunoglobu F;1-438/Domain: C region <CRE>
F;20-87/Domain: immunoglobulin homology <IM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;123-190/Domain: immunoglobulin homology <IM2>
F;228-291/Domain: immunoglobulin homology <IM3>.
F;330-400/Domain: immunoglobulin homology <IM4>
F;330-400/Domain: immunoglobulin homology <IM4>
F;164,200,245,275,374,411,415,425/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X07781
A;Note: the sequence was determined from the germline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Complete structure and organization of immunoglobulin A;Reference number: S00980; MUID:88328985; PMID:3138109 A;Accession: S01853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig mu chain C region, secreted (clone 3050) - horn shark
C;Species: Heterodontus francisci (horn shark)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 100/1; 206/1; 309/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Kokubu, F.; Hinds, K.; Litman, R.; Shamblott,
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1979-1988, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLT
                                                                                                                                                                                                                                                                                                                             WKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEV- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLLPPPSEE
KDGQHMESGFVTSPT--C----GVNGTFSATSRLTVPAREWFTNKVYTCQV--SHQGVTQ 197
                                                         ----LESPPGSSPSVQCRSPRGKN--IQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEF 195
                                                                                                                             RGESVWIKEIPDCKGDKVHPTVILTQSSSEEITSRRFATVLCSIIDFH---PESITVSWL
                                                                                                                                                                                             -----EDQKEEVQLLVFG--LTANSDTHLLQGQSLTLT-- 142
                                                                                                                                                                                                                                                             WKKDNEPITTG-----LKTYPSVLNKKGTYTQS-----SQLTITESEVGSSKIY-CEVR
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%;
                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 294; DB 1;
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 438;
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                                                                                                                                                                                                                                                                                                                                                                                              92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339
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A;Residues: 1-299 <a href="https://www.nib.com/residues">h;Cross-references: GB:X00353; NID:g1575; PIDN:CAA25100.1; PID:g1576</a>
A;Cross-references: GB:X00353; NID:g1575; PIDN:CAA25100.1; PID:g1576
C;Comment: This immunoglobulin belongs to the IgA-g subclass. It was isolated fro C;Complex: An immunoglobulin some cases, such as IgA and IgM, the subunits associate hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin; plasma F;86-152/Domain: immunoglobulin homology <IM1>
F;189-261/Domain: immunoglobulin homology <IM2>
F;189-261/Domain: immunoglobulin homology <IM2>
                                                                                                       A; Molecule type: DNA
A; Residues: 1-338 «BUR»
C; Superfamily: immunoglobulin C
C; Keywords: immunoglobulin
                                                                                                                                                                                                                                                              R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L. EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Knight, K.L.; Martens, C.L.; Stoklosa, C.M.; Schneiderman, Nuclelc Acids Res. 12, 1657-1670, 1984
A;Title: Genes encoding alpha-heavy chains of rabbit IgA: cha;Reference number: A02174; MUID:84144059; PMID:6322114
                                                                                                                                                                                                                       A;Reference number: S09264; MÜID:90076124; PMID:2512120 A;Accession: S09276
                                                                                                                                                                                                                                                                                                                                                     Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Jul-1999
C;Accession: A02174
                                                                                                                                                                                                   A; Status: not compared with conceptual translation
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Query Match
Best Local S
Matches 92
                                                                                       228-300/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 VPCPAPEPKSCDKTHTCP-----ELLGG--PSVFLFPPKPKDTLMISRTPEVTCVVVDVS
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l Similarity
92; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q--PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDSGSLTATISRGVVTP--PQVHLLPPPSEELALNEQVTLTCLVRGFSPKDVLVSWRHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPA-PIEKTISKAKGQPREPQVYTLPPSRDELTKN-QVSLTCLVKGFYPSDIAVEWESNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPEDAV-FTW--EPTNGNEPVQQRAQRDLSGCYSVSSVLPSSAETWKARTEFTCTVTHPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPVPFPDCCPANSCCTCPSSSSRNLISGCQPSLSLQRPDLGD-LLLGRDASLTCTLSGLK
  Conservative
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                                                                                       immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431
                    10.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 293; DB 1 31.7%; Pred. No. 2e-10;
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50;
                                                                                                                                region;
Score 292; DB 2;
Pred. No. 2.7e-10;
0; Mismatches 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 106;
                                                                                                                                immunoglobulin
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                                       Length 338;
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                                                                                                                                homology
Indels
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                                                                                                                                                                                                                                                                   sequence analysis
40;
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Gaps
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light (kap
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Ig alpha chain C region - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_cha
C;Accession: S09266
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning
A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09266
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S09266
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A;Residues: 1-352 <BUR>
A;Residues: 1-352 <BUR>
C;Superfamily: inmunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
C;Keywords: immunoglobulin
F;241-314/Domain: immunoglobulin homology <IMM>
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Best Local
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428
                                                                                                                                                                                                                         156
                                                                                                                                                                                                                                                                                                                                                           199 IVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 LTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKID 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
LSPG
                                                                                                                                                           APIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ-- 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKCKVSNKALPA-PIEKTISKAKGQPREPQVYTLPPSRDELTKN-QVSLTCLVKGFYPSD 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                           VPKDSFLVWKPLPEPGQEPTTYAVTSLLRVPAEDWNQGDSYSCVVGHEGLAEHFTQRTID 329
                                                                                                                                 GSITATISRGSLTP--PQVHLLPPPTEELALNALVTLTCLVRGFSPKDVLVSWTHNGTLV
                                                                                                                                                                                                                       AVFTWNPTNGNEFVQQST----QSYPCGCYSVSSVLPGCAEPWNAGTEFTCTVTHPEIEG
                                                                                                                                                                                                                                                                   VKENWY-VDGVEVHNAKTKPREEQYN-STYRVVSVLTVLHQDWLNGKEYKCKVSNKALP-
                                                                                                                                                                                                                                                                                                                 PTPCPCP-PITC----
                                                                                                                                                                                                                                                                                                                                                                                                       LHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLVSWRHQGQEVPEDSFLVWKSMPESSQDKATYAITSLLRVPAEDWNQGDTYSCMVGHEG 304
                                                                                     -PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAVEWESNGQ--PENNY---KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTCTLSGLKNPEDAV-FTW--EPTNGNEPVQQRAQRDLSGCYSVSSVLPSSAETWKARTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYNSVINESLPVPFPDCCPANSCCTCPSSSSRNLISGCQPSLSLQRPDLGD-LLLGRDAS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPG--PLSVSWTVNGENV---SAYNFPPAQSGTSGPYTACSELILPVTQCLGQKSAACHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAEHFTQRTIDRLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FTCTVTHPEIDSGSLTATISRGVVTP--PQVHLLPPPSEELALNEQVTLTCLVRGFSPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFKIDI----VPCPAPEPKSCDKTHTCP-----ELLGG--PSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin homology <IMM>
431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%; Score 292; DB 2; 31.2%; Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                                               -GEPSLSLQRPDIGD-LLLESNASLTCTLSGL--KDPEG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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330 RLAG

EPTFGKEPVQQSPQLDHCGCYSVSS

289 188

102

347

308 401

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Ig heavy chain precursor V region - ladyfish
C;Species: Elops saurus (ladyfish)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jul-2000
C;Accession: A34891
R;Amemiya, C.T.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 811-815, 1990
A;Title: Complete nucleotide sequence of an immunoglobulin heavy-chain gene and anal. A;Reference number: A34891; MUID:90138916; PMID:2105490
A;Accession: A34891
A;Accession: A34891
A;Residues: prelininary
A;Molecule type: mRNA
A;Residues: 1-568 < AME>
A;Cross-references: GB:M26182; NID:9213134; PIDN:AAA49238.1; PID:9213135
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Kcywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology < IMM>
                                                                                    Ig alpha chain C region - rabbit (fragment)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
C;Accession: S09265
R;Burnett, R.C.; Hanly, W.C.; Zhai, S.K.; Knight, K.L.
EMBO J. 8, 4041-4047, 1989
A;Title: The IgA heavy-chain gene family in rabbit: cloning and A;Reference number: S09264; MUID:90076124; PMID:2512120
A;Accession: S09265
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-357 <BUR>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin c region; Immunoglobulin homology
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Best Local S
Matches 92
    Query Match 10.7%;
Best Local Similarity 28.2%;
Matches 93; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TASSFLOASESQWKRLDGTFTCQFIQEGEITEQTVKYSSAEC-SPEAQIDAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PASDWDSGVVYSCAVHHETVMESVVKTIVRTTDSVSKKPTTVSLDLNVPQTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKSRWQQGNVFSCSVMHEAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQFDE-QKMISKLLIDYEEWKNRTEYTCKVEHSDLPSPLRTSYRRECGGKWQSPTVFILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK-AKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGGKTLSVSQLELQD-SGTWTCTVLQNQKKVE--FKIDIVPCPAPEPKSCDKTHTCPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATFACLATD-----FYPKGHSFKWLRDGKEVT-----DGIATLTECQKKGDKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGDFKSKAEFKCTTELGGKKT-----PVVIPKPEPPKPPRQPVLSIMTPSQEELTLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGSFLTKGPSKLNDRADSRRSLWDQGNFPLII--------KNLKIED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA-EQRNLSTVTLICYAKDFYPEQVLISWLVDDQPVETDVPTTEVVKTEGTYSVFSQLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ISPPTPEE-LFLQQTRTLTC-----KITGDVDGVRNVTWEVGSEVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE--VHNAKTKPRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.7%; Score 290; DB 2;
22.3%; Pred. No. 6.5e-10;
ative 78; Mismatches 152
      49;
    Score 289; DB 2; pred. No. 4.3e-10; p; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -HNHYTOKSLSLSPGLQLDETC
                                                                                                                                                                                                                                                                                                                                               #text_change 16-Jul-1999
                                          Length 357
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    Indels
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    66;
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  Gaps
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    14;
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C;Superfamily: immunoglobulin C region; immunoglobulin
F;230-302/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Chintalacharuvu, K.R.; Raines, M.; Morrison, S.L.
J. Immunol. 152, 5299-5304, 1994
A;Title: Divergence of human Jaha-chain constant region
A;Reference number: 156230; MUID:94246170; PMID:8189047
A;Accession: 156230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig alpha-2 chain - human (fra
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence
C;Accession: I56230
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C; Genetics:
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156230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                       168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189
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                        397
                                                                                                                                                                                                                                                                                   223
                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 VFGLTANSDTH------LLQG----QSLTLTLESPPGSSPSVQCRS-PRGKNIQGGKT 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402
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                                                                                                                                                                                                                                                                                                                                                                   169 LSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDI-VPCPAPEPKSCDKTHTCPELLGG
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                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                œ
VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG-----
                                                                                                                                                    GCYSVSSVLPGCAQPWNHGETFTCTAAHPELKTPLTANITKS-GNTFRPEVHLLPPPSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE----QYNSTYRVVS
                                                              LALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTTFAVTSILR
                                                                                                            LTKNQ-VSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLD-SDG--SFFLYSKLT
                                                                                                                                                                                          STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDB
                                                                                                                                                                                                                                                                                 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                           TTSSQLTLPATQCPDGKSVTCHVKHYTNSSQ---DVTVPCRVPPPPPPC-----C-----H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSGESVIFPPVPSPPSSLYTTYSLLRLPAEQCPEENSVACRVEHNNKGQDVTVPSPPACN
                                                                                                                                                                                                                                       PRISIHRPALED-LILGSEANLTCTLTGL-RDASGATFTWTPSSGK--SAVQGPPERDLC
                                                                                                                                                                                                                                                                                                                                                                                                                VFPLSLDSTPQDGNVVVACLVQGFFPQEPLSVTWSE---SGQNVTARNFPPSQDASGDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WNOGDSYSCVVGHEGLAEHFTOKTIDRLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSLTCLVKGFYPSDIAVEWESNGQ---PENNYKTTPPVLD---SDGSFFLYSKLTVDKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLPGCAVLWNAGTEFTCTVTHPEIEGDSLTGTISKDTGSLIPPQVHLLPPPSEELALNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLTVLHQDWLNGKEYKCKVSNKALPA-PIEKTISKAKGQPREPQVYTLPPSRDELTKNQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESTIEPPTTPTC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 286.5; DB 2
Pred. No. 5.7e-10;
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Db 287 VAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVMAEVDGTC 339
Search completed: August 3, 2004, 13:15:19
Job time: 16.7668 secs

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Result
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US-08-487-918-1
US-08-487-918-1
US-09-039-558-15
US-09-517-605-3
US-09-486-368-2
US-08-486-368-2
US-08-38-500-2
S223394-7
Sequence 5, Appli Sequence 29, Appli Sequence 29, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3
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US-08-472-888A-6
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                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/472,888A
FILING DATE: 07-JUN-1995
CLASSIFICATION 1424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/618,314
FILING DATE: 23-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/258001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
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APPLICANT: Walz, Gerd
TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS
TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 630 amino acids
                    TYPE: amino acid
STRANDEDNESS: unl
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US-08-457-918-7
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US-09-180-100-22
US-09-180-25-23
US-09-180-25-24
US-09-26-985-71
US-09-234-340A-71
US-09-234-340A-71
US-09-236-098-8
US-09-526-098-8
US-09-746-359A-54
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US-09-746-359A-54
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US-08-477-460B-4
                                                                                                                                                             Sequence 4, Application US/08477460B
Patent No. 6034223
GENERAL INFORMATION:
APPLICANT: PROGENICS Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOC
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
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Best Local Similarity
Matches 617; Conserv
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIn Release #1.24
                                                                                                                                  STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                  ZIP: 10112
                                                                                                                    STATE:
                                                                                                   COUNTRY:
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Pred. No. 5.1e-245;
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Best Local Similarity 68.9%;
Matches 437; Conservative 2
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FILING DATE: 07-AUG-1992
ATTORNEY/ACENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acids
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ORIGINAL SOURCE:
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FILING DATE: 07-UN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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STRANDEDNESS: un)
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                                                                                                           EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 531
                                                                                                                                                                                      ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 471
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                                                               PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 591
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                                                                                                                                                                                                                                                                                                    TFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNV------
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Pred. No. 7.3e-160;
5; Mismatches 58;
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APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.
FITTLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-IgG2
FITTLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CUURRENT ELIVING DATE: 1996-06-10
FARLIER APPLICATION NUMBER: DC7/US93/07422
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER FILING DATE: 1993-08-06
FEARLIER FILING DATE: 1992-08-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENING DATE: 1992-08-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENING DATE: 1992-08-07
FYPE: PRT
ORGANISM: Homo sapiens
US-08-379-516-4
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Patent No. 6083478
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                  PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 591
                                                                                                                                        EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
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                                                                                                                     EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
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RESULT 4
US-09-329-916-4
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Best Local Similarity
Matches 437; Conserv
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/477,46
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 07/927
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28.678
REGISTRATION NUMBER: 28.678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/329,916
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: N
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CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homo sapien CELL TYPE: lymphocyte
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                                                  TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240
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                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                     TWTCTVLQNQKKVEFKIDIVVLAF--AST-----KGPSV---FPLA---
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NON-PEPTIDYL MOIETY-CONJUGATED

CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES THEREOF

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Pred. No. 7.3e-160;
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                                                                                                                                                                                                                                                                                                                                                                                    Length 530;
                                                                                                                                                                                                                                                                                                                                              Indels 114;
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Patent No. 6187748
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APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IGG2
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                 APPLICATION NUMBER: 08/476,22
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3765
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
08/476,227
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,37
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                        SEQUENCE CHARACTERISTICS:
MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                 TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
                                                                                                LENGTH:
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                                                                           amino acid
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1185 Avenue of the Americas
                                                                                              530 amino acids
                                                                                                                                                                                (212) 391-0525
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; ORGANISM:
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US-08-485-372A-4
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US-09-409-006A-4
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Best Local Similarity
Matches '437; Conserv
ZIP: 10112
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                             APPLICANT: Progenics Pharmaceuticals, TITLE OF INVENTION: NON-PEPTIDYL MOIE TITLE OF INVENTION: CD4-GAMMA2 AND CD.
                                                                                                                                     NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                            STREET: 30 Rockefeller Plaza CITY: New York
                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                 592
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                                                                                                                                                                                                                                                                                                                    DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL
                                                                     USA
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                                                                                                                                                                NON-PEPTIDYL MOIETY-CONJUGATED CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES
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Pred. No. 7.3e-160;
5; Mismatches 58;
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acid
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APPLICATION NUMBER: US 07/927
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4121:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEPAX: (212) 977-9809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 29-SEP-199
CLASSIFICATION: 424
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ORIGINAL SOURCE:
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CELL TYPE:
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STRANDEDNESS: unl
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lymphocyte
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121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                   PSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPMLDSDGSFFLYSKLTV
                                                                                                                                                                                                     EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
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Pred. No. 7.3e-160;
Pred. No. 58;
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Best Local Similarity 68.9%; Pr
Matches 437; Conservative 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PSTEM: PC-DOS/MS-DOS
SOTTWARE: PSTEMIC Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,681
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Beaudry, Gary A.
APPLICANT: Meddon, Paul J.
APPLICANT: Meddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2 CHIMERAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 530 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 37690-II-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooper &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unl
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                               241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL 297
                                                                                                                                         121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFFLAFTVEKLTGSGELWW 240
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1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              530 amino acids
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                                                                                                                                                                                                                                                                                                                                                           Score 2116; DB 4;
Pred. No. 7.3e-160;
5; Mismatches 58;
-PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 255
                                                                                                                                                                                                                                                                                                                                                                                               Length 530;
                                                                                                                                                                                                                                                                                                                                                             Indels 114;
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RESULT 8 PCT-US93-00 FCT-US93-00 FCT-US93-	Db Qy	Db Qy	D Qy	ОУ	9g 9g	Qy dd
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US-08-477-460B-2
                                                                                                                                                                                                                                                                             Sequence 2, Application US/08477460B
PATENT NO. 6034223
GENERAL INFORMATION:
APPLICANT: Progenice Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES,
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                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PM PC POS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA;
                                                                                                                                                             STREET: JOIK
CITY: New York
TTATE: New York
TTSA
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: 0
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
             APPLICATION NUMBER: US/0:
FILING DATE: 07-JUN-1995
                                                                                                                                                 ZIP: 10112
CLASSIFICATION:
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                             US/08/477,460B
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5; Mismatches 58; Indels 114;
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ORIGINAL SOURCE:
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CELL TYPE:
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STRANDEDNESS: uni
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                                                                      VFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                       QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                                                                VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN
                                                                                                                                                                                                                                              LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
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lymphocyte
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APPLICANT: Allaway, Graham P.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: No. 6083478-Peptidyl Moiety-Conjugated CD4-Gamma2 and CD4-
TITLE OF INVENTION: Immunoconjugates and Uses Thereof
FILE REFERENCE: 41215-A-PCT-US
CURRENT APPLICATION NUMBER: US/08/379,516
CURRENT FILING DATE: 1996-06-10
EARLIER APPLICATION NUMBER: PCT/US93/07422
EARLIER FILING DATE: 1993-08-06
EARLIER FILING DATE: 1993-08-06
EARLIER FILING DATE: 1993-08-07
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Homo Sapiens
US-08-379-516-2
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Best Local Similarity
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                                                                                        QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                                                                                                                                                                                                                    LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
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                                 VFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                                                                                                                          VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 540
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                                                                     QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                        VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN
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RESULT 11

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;-Sequence 2, Application US/09329916
; Patent No. 6177549
; GENERAL INFORMATION:
APPLICANT: Progenics Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
; TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IgG2 IMMUNOCONJUGATES,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                            Matches 410;
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TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: 08/477,46

FILING DATE: 07-UN-1995

APPLICATION UMBER: US 07/927

FILING DATE: 07-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION UMBER: 28,678

REFERENCE/DOCKET NUMBER: 4121

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: unl
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RESULT 12
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APPLICANT: Beaudry, Gary A.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: CD4-GAMMA2 CD4-IgG2
                                                                                                                                                                                           APPLICATION NUMBER: 08/476,227
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 2,678
REFERENCE/DOCKET NUMBER: 3,678
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                      TYPE: amino acid
STRANDEDNESS: unl
                              ORGANISM:
                                                                           TOPOLOGY: unknown
                                                                                                                                                                    TELEX:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
            CELL TYPE:
                                                                                                                   LENGTH: 432 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Cooper & 1185 Avenue
                                                                                                                                                                                   (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                           homo sapien
              Lymphocyte
                                                                                       unknown
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of the Americas
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RESULT 13
US-09-409-006A-2
; Sequence 2, Application US/09409006A
; Patent No. 6342586
; GENERAL INFORMATION:
Drogenics Pharmaceuti
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/409,006
FILING DATE: 29-SEP-1999
                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                      STREET: JUNE YORK CITY: New York YORK
                                                                                                                                                                                                                                           APPLICANT: Progenics
TITLE OF INVENTION: N
                                                                                                                                                                                                              NUMBER OF SEQUENCES: S
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30 Rockefeller Plaza
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NON-PEPTIDYL MOIETY-CONJUGATED
CD4-GAMMA2 AND CD4-IgG2 IMMUNO
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                 US/09/409,006A
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Best Local 9
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REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41215-A-PCT/JPW/AJM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 42523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 0.
FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
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ORIGINAL SOURCE:
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               VFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                 VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN
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VESCSVMHEALHNHYTQKSLSLSPG
                                                          QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
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Pred. No. 1.8e-155;
2; Mismatches 9;
431
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; ORGANISM: |
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US-08-484-681-2
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US-08-484-681-2
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APPLICANT: Beaudry, (
APPLICANT: Maddon, Pa
APPLICANT: MADDON, PA
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                        Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3769
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Relea
CURENT APPLICATION DATA:
APPLICATION UMBER: US/(
FILING DATE: 07-UUN-199;
CLASSIFICATION: 435
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ORIGINAL SOURCE:
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CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 432 amino acids TYPE: amino acid STRANDEDNESS: unknown
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     301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
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                                                                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                        QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFERKCCV----
                                                                                                                                                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQ1K
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1185 Avenue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                       60.3%; Score 2059; DB 4; ilarity 65.6%; Pred. No. 1.8e-155; Conservative 12; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo sapien
: lymphocyte
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CD4-GAMMA2 CD4-IgG2 CHIMERAS
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                                                                                      ; CELL TYPE: PCT-US93-07422-2
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PCT-US93-07422-2
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                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 4121
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-950
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application PC/TUS9307422
GENERAL INFORMATION:
APPLICANT: PROGENICS Pharmaceuticals, Inc.
TITLE OF INVENTION: NON-PEPTIDYL MOIETY-CONJUGATED
TITLE OF INVENTION: CD4-GAMMA2 AND CD4-IGG2 IMMUNOCONJUGATES, AND USES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                            Matches 410;
                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07422
FILING DATE: 1930806
CLASSIFICATION:
                                                                                                                TOPOLOGY: unkn
MOLECULE TYPE: p
ORIGINAL SOURCE:
ORGANISM: homo
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 07-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                            Local Similarity
                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                      TYPE: amino acid
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1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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T: 30 Rockefeller Plaza
New York
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                              Conservative
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                            12;
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                           Score 2059; DB 5;
Pred. No. 1.8e-155;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PPCPAPP------VAGPSVF
                                                      Length 432;
                           Indels 194;
                           Gaps
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RESULT 16
US-08-417-495-6
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Patent No. 5843728
GEMERAL INFORMATION:
APPLICANT: Seed, Brian et al.
                                                            APPLICATION NUMBER: US
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                 CUMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM PC. DOS (Version SOPTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBERS
                                                                                                                                                                                                                                                                                                                                                                                              STATE: USA
COUNTRY: USA
COUNTRY: 02110-2804
TTP: 02110-2804
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PS/2 model 50
OPERATING SYSTEM: IBM P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCE: ADDRESS:
CORRESPONDENCE ADDRESS:
Pish & Richardson
Processes:
Procedure Address
Pr
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: E
FILING DATE: APPLICATION NUMBER:
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   US/07/847,566
                                                                    US/08/203,866
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US-08-284-391B-6
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                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Seed, Babak
APPLICANT: Romeo, Charles
APPLICANT: Romeo, Charles
APPLICANT: Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
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Best Local S
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INFORMATION FOR SEQ ID NO:
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LENGTH: 532 amino acids
TYPE: amino acid
TOPOLOGY: linear
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
COMPUTER READABLE FORM:
             STREET: 176 F.
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
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Local Similarity 98.3%;
nes 397; Conservative
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REGISTRATION NUMBER: 30,162
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                                                                            176 Federal Street
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RESULT 18 US-09-218-950-6

Sequence 6, Application US/09218950 Patent No. 6284240

GENERAL INFORMATION:
APPLICANT: Seed, B:
APPLICANT: Banapou:
APPLICANT: Romeo, (

Romeo, Charles Seed, Brian

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Matches 397;
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Best Local Similarity 98.3%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,39:
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,56:
FILING DATE: 07-MAR-1992
APPLICATION NUMBER: 07/665,96:
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 078
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 532 amino acid
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TELEX:
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                       LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSC 404
LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHA---DPKLC
                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVMV
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                                                                             LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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Pred. No. 1.56
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP ADDRESSEE: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US/09/218,950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/1
FILING DATE: 14-FEB-1994
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TOPOLOGY: 11r
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                                                                                                                                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQCGKTLSVSQLELQDSG 180
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                                                                                                                                                       TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                       LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
                                                                QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                              QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
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LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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98.3%;
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Pred. No. 1.5
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Matches
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GENERAL INFORMATION:
APPLICANT: The General Hospital Co
TITLE OF INVENTION: Redirection of
TITLE OF INVENTION: Chimeras
                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.4
COMPUTER: IBM PS/2 Model 50Z oloperating System: IBM P.C. DOS
SOFTWARE: Wordperfect (Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 19920306
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/66
FILING DATE: MARCh 7, 199
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T.
NAME: CLARK, PAUL T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                        Local Similarity
les 397; Conserv
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emrser: 225 Franklin Street
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               QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
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AMINO ACID
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QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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                                                         TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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98.3%;
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Pred. No. 1.5e-153;
1; Mismatches 3;
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                                                                                                                                                                                                        Matches 397;
                                                                                                                                                                                                                      Query Match
Best Local
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 amino acids
TYPE: amino acid
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TITLE OF INVENTION:
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TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/247001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/665
FILING DATE: March 7, 1991
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OPERATING SYSTEM: IBM PC.C DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette,
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ADDRESSEE: Fish & Richardson
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CLASSIFICATION:
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                        LVFGLTANSDTHLLQGQSLTLITLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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Pred. No. 1.5e-153;
1; Mismatches 3;
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Patent No. 5843728
GENERAL INFORMATION:
              Best
 Matches
                             Query Match
                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOPTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 27
                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                             MOLECULE TYPE:
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TELEFAX: 200154
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ZIP: 021
             Local
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225 Franklin Street
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59.7%;
llarity 98.3%;
Conservative
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Score 2036.5; DB 2;
Pred. No. 1.7e-153;
1; Mismatches 3;
 Indels
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COUNTR.

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ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/284,391B

TITING DATE: 02-AUG-1994
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US-08-284-391B-4
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APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldema
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 575 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF
TITLE OF INVENTION: CELLS BY CHIMERIC CD4
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
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CITY: Bo
STATE: M
COUNTRY:
                                                                          TELEPHONE:
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176 Federal Street
                                                                            617-428-7045
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RESULT 23
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Best Local Similarity
Matches 397; Conserv
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STRANDEDNESS: sin
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                                                           LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHA---DPKLC
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98.3%;
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Pred. No. 1.7e-153;
1; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Seed, B
APPLICANT: Banapou
APPLICANT: Romeo,
APPLICANT: Kolanus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
PRIOR APPLICATION NUMBER: US/08/284,3
APPLICATION NUMBER: US/08/284,3
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BE
                                                                                                                                                                                                                                                                    STREET:
CITY: Bo
STATE: M
COUNTRY:
ZIP: 021
                                                                                                             CLASSIFICATION:
                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                      02110
                                                                                                                                                                                                                                                                                                                   Boston
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176 Federal Street
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Banapour, Babak
Romeo, Charles
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                                                                        US/08/284,391
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RESULT 24
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                                                                                                                                                                               Sequence 4, Application PC/TUS9201785
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor
TITLE OF INVENTION: Chimeras
NUMBER OF SEQUENCES: Chimeras
ADDRESSEE: Fish & Richardson
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APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
COMPUTER: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
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                                                                                                                 COUNTRY:
                                                                                                                                                  ADDRESSEE: F18n ....
empRET: 225 Franklin Street
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Local Similarity 98.3%;
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TOPOLOGY: lir
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Pred. No. 1.7e-153;
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RESULT 25 PCT-US95-00454-4

Sequence 4, Application PC/TUS9500454
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Targeted Cytol
TITLE OF INVENTION: Cells by Chime
TITLE OF INVENTION: Bearing Cells

Targeted Cytolysis of HIV-Infected Cells by Chimeric CD4 Receptor-

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson

STREET:

225 Franklin Street

Boston

STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:

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TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: AMINO ACID
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APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 00786/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
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361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSC 404
                                                                       301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                          301 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                            241 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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98.3%;
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Pred. No. 1.7e-153;
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Sequence 5, Application U.
Patent No. 5843728
GENERAL INFORMATION:
APPLICANT: Seed, Brian
TITLE OF INVENTION: RA
                                                                                                RESULT 26
US-08-417-495-5
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 575 amino acids
TYPE: amino acid
TOPOLOGY: linear
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NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
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COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordporfect (Version 5.0)
CURRENT APPLICATION DATA:
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TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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FILING DATE: March 7, 1991
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Similarity 98.3%;
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Receptor
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Pred. No. 1.7e-153;
                  of Cellular Immunity
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US-08-417-495-5
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
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NAME: Clark, Paul T.
REGISTRATION UNMER: 30,162
REFERENCE/DOCKST NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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APPLICATION NUMBER: 1
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TYPE: amino acid
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FILING DATE:
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2804
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Similarity 98.0%;
LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSC 404
                                                                                          LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                   QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                               QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                             LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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Pred. No. 2.60
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Patent No. 5851828
GENERAL INFORMATION:
APPLICANT: Seed, Brian
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                     Matches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 462 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Elbing, Karen L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                               121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                     TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEESFPLAFTVEKLTGSGELWW 240
                                                                                                                                                                                                                           MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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ER: 00786/247001
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US-09-218-950-5
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       Query Match
Best Local Similarity
Matches 396; Conserv
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APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/195
FILING DATE: 14-FBB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US/08/284,391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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ADDRESSEE: Clark & Elbing LLP
                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                  NAME: Elbing, Karen L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 02-AUG-1994
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                                                                                                                  TOPOLOGY:
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linear
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                      59.5%;
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       2;
       Score 2032.5;
Pred. No. 2.6e
2; Mismatches
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5; DB 3;
2.6e-153;
3;
                                           Length
                                           462;
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       Gaps
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                                                                      TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-01785-5
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Sequence 5, Application:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

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REQUENCES: 27
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PCT-US92-01785-5
Query Match 59.5%;
Best Local Similarity 98.0%;
Matches 396; Conservative
                                                                                                                                                  TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" biskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01785
FILING DATE: 19920306
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                          NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/119002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/6.
FILING DATE: March 7, 19.
ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Fish & Richardson
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STATE: MA
COUNTRY: USA
ZIP: 02110-28
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                                                                                                                                           LENGTH:
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Score 2032.5; DB 5
Pred. No. 2.6e-153;
2; Mismatches 3;
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                               DB 5;
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHA---DPQLC
                                                           LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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RESULT 30
PCT-US95-00454-5
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GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                   APPLICATION UNMBER: 07/665,96
FILING DATE: March 7, 1991
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                               APPLICATION NUMBER: POFILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07
FILING DATE: March 6,
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOPTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NIMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PS/2 Model 50
OPERATING SYSTEM: IBM P.C.
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ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
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TITLE OF INVENTION:
                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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27
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Cells by Chimeric CD4 Receptor-
Bearing Cells
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/847,566
PULING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
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TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00454-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5851828
GENERAL INFORMATION:
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Best Local 9
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APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                             STREET: 176 F
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Local Similarity 98.0%;
APPLICATION NUMBER: 07/8 FILING DATE: 06-MAR-1992 APPLICATION NUMBER: 07/6
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176 Federal Street
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Pred. No. 2.6e-153;
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Sequence 29, Application US/0921895
Patent No. 6284240
GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CY
TITLE OF INVENTION: CELLS BY CH
NUMBER OF SEQUENCES: 53
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US-09-218-950-29
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Matches
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                 COUNTRY: US
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                   CITY: Bost
STATE: MA
                                                                                                                     ADDRESSEE: Clark & Elbing LLP STREET: 176 Federal Street
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RESULT 33
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                                                   Sequence 4, Application US/08466368 Patent No. 6093539 GENERAL INFORMATION:
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Best Local Similarity 100.0%;
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FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/2.
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LENGTH: 398 amino acids
TYPE: amino acid
   APPLICANT:
APPLICANT:
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TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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PRIOR APPLICATION DATA:
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SOFTWARE: FASUSEQ for Windows Version
CURRENT APPLICATION DATA:
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TOPOLOGY: linear
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Maddon, Paul J.
Littman, Dan R.
Chess, Leonard
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/466
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2457
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weise, Robin
APPLICANT: McDougal, J. S.
TITLE OF INVENTION: DA ENCODING THE T CELL SURFACE PROTEIN
TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TRI
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 458 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
STATE: New York
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361
                 361 LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
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RESULT 34 US-08-328-500-9

Sequence 9, Application US/08328500

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/24577-CY
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Maddon, Paul J.
APPLICANT: Axel, Richard
APPLICANT: Sweet, Richard W.
APPLICANT: Arthos, James
TITLE OF INVENTION: DERIVATIVES
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ADDRESSEE: Cooper & Dunham
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STATE: New York
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                                LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
                                                                                                   LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                  LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWV
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INPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
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99.7%;
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Pred. No. 2.1e-152;
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RESULT

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                                                                                                                                                                                                                                                                                                                                                             Matches 392;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION UMBER: 07/250785
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/104329
APPLICATION UMBER: 07/104329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: patin (Generatech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 44
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UFILING DATE: 02-MAY-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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MEDIUM TYPE: 5.25 inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 402 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415/225-18
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                       241
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QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
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                                                            TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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Pred. No. 3.6e-152;
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US-08-457-918-1
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                                                             Query Match
Best Local S
Matches 392
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                          NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 07/104329 FILING DATE: 02-OCT-1987 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 28-SEP-1
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
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ADDRESSEE: Genentech,
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                                                               Local Similarity hes 392; Conserv
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FILING DATE: 1-JUN-1995
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CITY: South San Francisco
STATE: California
                                                                                                                                               TOPOLOGY:
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MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                               Conservative
                                                                                                                                               linear
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                                                                            59.1%;
99.7%;
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                                                             Score 2017; DB 3;
Pred. No. 3.6e-152;
0; Mismatches 1;
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                                                                                            Length 402;
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                                                             Gaps
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RESULT 37
US-09-039-555B-15
US-09-039-555B-15
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15
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APPLICANT: Mueller, Rolf
APPLICANT: Saddlacek, Hans-Harald
TITLE OF INVENTION: PREPARATION AND US
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION UNMBER: DE 197
APPLICATION NUMBER: DE 197
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,76
REFERENCE/DOCKET NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K STREET: Washington
                                TOPOLOGY:
                                               STRANDEDNESS
                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/039,555B FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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             ECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B: Foley & Lardner
                                                                                   458 amino acids
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SYSTEM: PC-DOS/MS-DOS
                                  linear
                                                                                                                                                                              (202) 672-5300
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Best Local S
Matches 392
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APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: wan Kooyk, Yvette
APPLICANT: van Kooyk, Yvette
APPLICANT: of invention: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09517605 Patent No. 6391567
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 3
LENGTH: 458
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                                                                                                                            | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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Pred. No. 6.3e-152;
0; Mismatches 2;
                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                   Score 2007; DB 4; Length 458; Pred. No. 2.7e-151;
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TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-466-368-2
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                                                                                                                                                                        Query Match
Best Local Similarity
Matches 389; Conserv
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0,

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,368

FILING DATE: 06-UUN-1995

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: McDougal, J. S.
TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPET & DWALL.
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STREET: LILL
CITY: New York
CTATE: New York
TISA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: White, John P. REGISTRATION NUMBER: 28,678
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                                  ILGNQGSSLTKGPSKLNDRADSRRSLWDQGNFPLIIRNLKIEDSDTYICEVEDQKEEVQL
                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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1185 Avenue of Americas
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Chess, Leonard
Axel, Richard
                                                                                                                                                                                                                                                                                                                   394 amino acids
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Littman, Dan R.
                                                                                                                                                                               Conservative
                                                                                                                                                                                          58.6%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version
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                                                                                                                                                                          Score 2001; DB 3;
Pred. No. 6.6e-151;
Nd gmatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                               24577-E1-B/JPW/AKC
                                                                                                                                                                                                             Length 394;
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; Sequence 2, Application US/08328500
; Patent No. 6673896
; GENERAL INFORMATION:
; APPLICANT: Maddon, Paul J.
; APPLICANT: Axel, Richard M.
APPLICANT: Sweet, Richard W.
; APPLICANT: Arthos, James
; TITLE OF INVENTION: DERIVATIVES O
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US-08-328-500-2
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APPLICATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/24577-CY
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                              Query Match
Best Local S
Matches 389
                                                                                                                                                                                             LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
:-08-328-500-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSE: Cooper & Dunham
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 1036
                                                                                                                                                                                                                                                                          TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,500
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MEDIUM TYPE: Floppy disk
                                                                                                                                Local Sim
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                                                                                                                                             h 58.6%;
Similarity 98.7%;
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ILGNOGSSLTKGPSKLNDRADSRRSLWDQGNFPLIIRNLKIEDSDTYICEVEDQKEEVQL
                    ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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                                                                                                                                Conservative
                                                                                                                                            Score 2001; DB 4;
Pred. No. 6.6e-151;
                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Version
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                                                                                                                                                             Length 394;
                                                                                                                              Indels
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RESULT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID
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APPLICANT: WALLNER, BARBARA
TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING
LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
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Matches 388;
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:7:
                      361
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                                                                                                                  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
             LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV 394
                                                                                                 GQERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                               LEAKTGKLHQEVNLVVMRHTQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWV
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                                                                LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV
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                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                   58.3%;
                                                                                                                                                                                                                                                                                                                                                     Score 1989; DB 6;
Pred. No. 7.4e-150;
0; Mismatches 6;
394
                                                                                                                                                                                                                                                                                                                                                                              Length 458;
                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                      0
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RESULT 42 5223418-2 ; Patent No.

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RESULT 43
US-08-236-311-4
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TITLE OF INVENTION: METHOD OF IMPROVING THE YIELD OF ;HETEROLOGOUS PROTEINS PRODUCED BY STREPTOMYCES LIVIDANS NUMBER OF SEQUENCES: 2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/589,979
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ARCURI, EDWARD J.; BRAWNER, MARY E.; DONOVAN,
APPLICATION NUMBER: 07/936190 FILING DATE: 26-AUG-1992
                                                                       APPLICATION NUMBER: US/08/236,311 FILING DATE: 02-MAY-1994
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-SEP-1990 NO:2:
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South San Francisco
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWTCTVLQNQKKVEFKIDIVVLAFGKASSIVYKKEGEQVEKSFPLAFTVEKLTGSGELWW
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ilarity 97.5%;
Conservative
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Pred. No. 6.2e-147;
0; Mismatches 10;
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Sequence 4, Application US/08457918
Patent No. 6117655
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variar
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

J. Variants

STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California

COUNTRY:

USA

94080

US-08-457-918-4

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Best Local Similarity
Matches 369; Conserv
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 434 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 28-SEP-PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 18-FEB-
PRIOR APPLICATION DATA:
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TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
416 IKVLPTWSTP
                                                                                                    324 KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESN
                                    384 IKVLPTWSTP
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                                                                                                                                                                        264 KRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQ
                                                                                                                                                                                                                                236 FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 QGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 434 amino acide amino acid
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                                                                          KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWYLNPEAGMWQCLLSDSGQVLLESN
                                                                                                                                                      KRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQ
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Pred. No. 3.9e-143;
0; Mismatches 1;
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Best Local S
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TELEPHONE: 415/225-8228
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/842
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA: 07/250
APPLICATION NUMBER: 07/250
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA: APPLICATION DATA: 07/104
APPLICATION UNMBER: 07/104
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: P0444P1C3
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FILING DATE: 26-AUG-1992
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
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amino acid
XGY: linear
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                        IKVLPTWSTP 393
                                                                                                                                                  KRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQ 323
                                                                                                                                                                                                                   FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV 263
                                                                                                                                                                                                                                                                                   ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA 203
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IKVLPTWSTP 425
                                                                                                                                                                                                FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV
                                                                                                                                                                                                                                                                  ESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA
                                                              KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWVLNPEAGMWQCLLSDSGQVLLESN
                                                                                              KNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESN 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jeffrey S.
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99.7%;
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Pred. No. 3.9e-143;
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Best Local S
Matches 367
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APPLICANT: Wang, Chang Y
ITITLE OF INVENTION: Anti
TITLE OF INVENTION: Anti
TITLE OF INVENTION: Prot
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Applic
Patent No. 5912176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/657,149
FILING DATE: 03-June-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Mari
STREET: 345 Par
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 433 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/01
FILING DATE: 28-Feb-1997
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                   LTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIK 385
                                                                                                                                                                                                                                                                        LMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTUTLES
                                                                                                                                                                                                                                                                                                                                            NKVVLGKKGDTVELTCTASQKKSIQFHWKNWNQIKILGNQGSFLTKGPSKLNDRADSRRS
                                                                                     VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN
                                                                                                                                      KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWIIFDLKNKEVSVKR
                                                                                                                                                                                                                                                                                                            LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES
                                                                                                                                                                                                                               PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ
                                                                                                                                                           KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKR
                                                                                                                                                                                                        PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ
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                                                                   VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN
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Antigen Complex for Pre- and
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Pred. No. 3.5e-142;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 433;
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HIV Primary Isolates
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US-08-808-374-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5961976
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/657,149
FILING DATE: 03-June-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Antibody Against a Host Cell
TITLE OF INVENTION: Antigen Complex for Pre- and
TITLE OF INVENTION: Protection from Infection by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: ami
                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                     181
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                    266
                                                                                    206
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                                                                                                                                                                                                                                                                                                                      367;
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                                                                                                                                                                                                                                                                      26 NKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRS
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                                                                                                                                                                                                                                                                                                                                    Similarity
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    433 amino acids
amino acid
    DGY: linear

VTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKN
                                                                                                                                                PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ 205
                                                                                                                                                                                    LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES
                                                                                                                                                                                                                    LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES
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                                                                                KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKR
                                                                                                                    PPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQ
                                                                                                                                                                                                                                                       NKVVLGKKGDTVELTCTASQKKSIQFHWKNWNQIKILGNQGSFLTKGPSKLNDRADSRRS
                                                     KASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWIIFDLKNKEVSVKR
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Pred. No. 3.5e-142;
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                                                                                                                                                                                                                                                                                                                                                   Length 433;
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HIV Primary I
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US-09-100-409A-1
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GENERAL INFORMATION:
                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 433 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wang, Chang Yi TITLE OF INVENTION: PEPTII TITLE OF INVENTION: PREVEN TITLE OF INVENTION: IMMUNE
                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pepi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
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                                                                                                                                                                                                          366;
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                                                                                                           87 WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP 146
                                                                                                                                                                  27 KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL
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                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVMVLNPBAGMMQCLLSDSGQVLLESNIK
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 ASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRV 266
                                                    PGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQK 206
                                                                                          WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESP
                                                                                                                                                 KVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL
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                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                     Length 433;
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Sequence 17, Application US/08630172
PATENT NO. 6060054
GENERAL INFORMATION:
APPLICANT: Staerz, Uwe
TITLE OF INVENTION: NOVEL PRODUCT AND PRO
TITLE OF INVENTION: LYMPHOCYTE VETO
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  RESULT 49
US-08-630-172-17
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5171838-13
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APPLICANT: CHIBA, YUKINOBU
TITLE OF INVENTION: LEUJA BINDING PEPTIDES
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/526,921
FILING DATE: 22-MAY-1990
SEQ ID NO.13:
LENGTH: 433
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BEST LOCAL Similarity 91.2%;
Matches 342; Conservative
                STREET:
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Denver
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                                                                                                                                                                                                                                                                 LESNIKVLPTWSTPV 394
                                                                                                                                                                                                                                                                                                                                TQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NQIKILGNXGSF-LTKGPSKLNDRADS-----RRSEEVQLLVFGLTANSDTHLLQGQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LWDQGNFPLIKNLKIED-SDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSL 139
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                            E: Sheridan Ross & McIntosh
1700 Lincoln Street, 35th Floor
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Pred. No. 1.6e-126;
5; Mismatches 13;
                                                                                                          PROCESS
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; MOLECULE TYPE: US-08-630-172-17
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APPLICATION NUMBER: US/08/630,172
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 863-022
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPAX: (303) 863-0223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 410 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                 566 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                        ALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ 565
                                                                                                                                                                SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK 505
                                                                                                                                                                                                                   PCP----PCKCPA-----PNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDV
                                                                                                                                                                                                                                        VLPTWSTPVPCPAPEPKSCDKTHTCPELIGGPSVFLFPPKFKDTLMISRTPEVTCVVVDV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLES
TELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
                                                                       DLPAPIERTISKPKGSVRAPQVYVLPPP-EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGK
                                                                                                                                           SEDDPDVQISWFVNNVEVHTAQTQTHREDYNSRLRVVSALPIQHQDWMSGKEFKCKVNNK
                                                                                                                                                                                                                                                                                           -----GPT-----IK 186
                                                                                                                                                                                                                                                                                                                             LTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIK 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1585.5; DB 3; ; Pred. No. 7.3e-118; 33; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2879-36
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Application US/09375419

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GENERAL INFORMATION:
APPLICANT: Staerz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.4%; Score 1585.5; DB 3; Best Local Similarity 54.2%; Pred. No. 7.3e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/375,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 410 amino acids
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
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                   386 VLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV 445
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                                                                                                                                  ---EPR-----
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1700 Lincoln Street, 35th Floor
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 --PCKCPA--
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 - PNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDV
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                                                                                                                                                    ; Patent No. 5223394
; APPLICANT: WALLNER, BARBARA
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING
; LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
;LINKAGE SIGNAL SEQUENCES: 12
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
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5223394-11
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TITLE OF INVENTION: RECOMBLUANT DNA MOLECULE COMPRISING
LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
LINKAGE SIGNAL SEQUENCE
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;SEQ ID NO:11:
                                                                                                          SEQ ID
 Matches 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 268;
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Best Local Similarity
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 10-APR-1989
                                                                                                                        APPLICATION NUMBER: FILING DATE: 10-APR
                                                                                         LENGTH: 295
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                                                                                                           NO:9:
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   Conservative
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                  39.98;
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Score 1363; DB 6;
Pred. No. 2.2e-100;
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Pred. No. 9.7e-101;
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                                    Length 295;
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1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

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RESULT 53
US-08-284-391B-33
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                                          US-08-284-391B-33
    Query Match
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                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: ETHIC EAVEL!
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APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldem
                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
LENGTH: 254 amino acid
                                                                                                                                                                                                                           NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FABUSEQ for Windows Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                          TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/284,391B FILING DATE: 02-AUG-1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: MA
                                                                                              STRANDEDNESS:
                                                                                                                  TYPE: amino acid
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    Application US/08284391B
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                                                                                                                                   254 amino acids
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                                                          protein
                                                                                              single
    39.2%;
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  Score 1338.5;
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  <u>ب</u>
Length 254;
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RESULT 54
US-09-218-950-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Banapour, Lander APPLICANT: Romeo, Charles APPLICANT: Kolanus, Waldemar APPLICANT: Kolanus, Waldemar TITLE OF INVENTION: CELLS BY CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Seed, 1
               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                             APPLICATION NUMBER: 08/195
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08
APPLICATION NUMBER: US/08
FILING DATE: 02-AUG-1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                           NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                                 TELEFAX: 617-428-7045
                                                                                     TELEPHONE:
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version
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                                                                                     617-428-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOLYSIS OF HIV-INFECTED CHIMERIC CD4 RECEPTOR- BEARING CELLS
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Sequence 8, Application US/09313942

Patent No. 6472179

Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: AND USING

FILE REFERENCE: REG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT APPLICATION NUMBER: 09/311,942

PRIOR APPLICATION NUMBER: 09/311,942

PRIOR APPLICATION NUMBER: 09/311,942

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1999-05-19

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 8

LENGTH: 592

TYPE: PRT

ORGANISM: Homo sapiens
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-218-950-33
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Matches
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Best Local Similarity 98.0%;
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                     7 Match 37.3%; Score 1275; DB 4; Length 592;
Local Similarity 47.3%; Pred. No. 5.9e-93;
nes 308; Conservative 53; Mismatches 160; Indels 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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166 QYSQESQKFSCQLAVPEGDSSFYIVSMCVASSVGSKFSKTQTFQ---GCGILQPDPPANI 222
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                                                                                                                                                                                                                26 PAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW-------VLRKPA----
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                                   LQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGEL-----
                                                                       PLSN------VVCEWGPRSTPSLTTKA----
                                                                                                                                          -AGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYRAGRPAGTVHLLVDVPPEEPQLSCFRKS 125
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                                                                                                                                                                              RADSRRSLWDQGNFPLIIKNLKIEDSDTYICE-----VEDQKEEVQLLVFGLT 126
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                                                                       ----VLLVRKFQNSPAEDFQEPC 165
                                                                                                                                                                                                                                                                                         Indels 130;
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246 VERSPHRPILQAGLPANKTVALGSNVEFMCKV	망
316 VMRATQLQKNLTCEVWGPTSPKLMLSLKLE 345	δ δ
195 FKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDV 245	뭕
261 VSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGK	ρ Q
b 167LKNGKE 194	Дb
203 AFQKASSIVYKKEGEQVEFSE	δ
114 FSVNVSDALPSSEDDDDDDSSSEEKETDNTKPNPVAPYWTSPEKMEKK	ఠ
162NIQGGKTLSVSQL	δõ
55 CRIRDDVQSINWIRDGVQLAESNRTRITGEEVEVQ-DSVPADSGLYACVTSSPSGSDTTY 113	da
109	Ş
Query Match 36.4%; Score 1243; DB 4; Length 622; Best Local Similarity 48.3%; Pred. No. 2.2e-90; Matches 299; Conservative 47; Mismatches 119; Indels 154; Gaps 23;	
TYPE: PRT ORGANISM: Homo sapiens 5-09-499-846-2	$\bar{\mathbf{o}}$
NO 2 H: 622	
12000-	
1/195012 (5784- JMBER: US/09/499,846	
APPLICANT: KAVANAUGA EC AL. TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUSION	
Patent No. 6656728 GENERAL INFORMATION:	
SULT 56 -09-499-840 Seguence 2	E E
541	뭕
Y 575 PVLDSDGSFELYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625	Ş
481 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 540	망
515	Ş
5 421 NWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 480	DЬ
455	Ş
361 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 420	당
400 EPKSCDKTHTC	Ş
316 TESRSPPAENEVSTPMQALTTNKDDDNILFRDSANATSLPVQDAG 360	밁
344 LENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQ	Ş
279 IH	문
284	Ş
223 TVTAVARNERWLSVTWQDEHSWNSSFYRLRFELRYRAERSKTFTTWWVKDLQHHCV 278	밁
239WWQAERASSKSW-ITFDL	Ş

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APPLICANT: Cerretti, Douglas P.
APPLICANT: Borgee, Luis G.
APPLICANT: Borgee, Luis G.
APPLICANT: Fanslow, III, William C.
APPLICANT: Fanslow, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/590,656
CURRENT FILING DATE: 2900-06-07
PRIOR APPLICATION NUMBER: 60/137,889
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 704
TYPE: PRT
ORGANISM: Homo sapiens
US-09-590-656-2
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Best Local
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Patent No. 641393
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240; Conservation
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KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
                                                           IEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY 570
                                                                                                                                           EVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP 510
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                                                                                                                                                                                                                                                                                                                       9;
                                                                                                                                                                                                                                                                                                                       Score 1237; DB 4; Length 704;
Pred. No. 7.9e-90;
9; Mismatches 12; Indels 3
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RESULT 58 US-09-733-764-2

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GENERAL INFORMATION:
APPLICANT: KAVANAUGH et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FU
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
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APPLICANT: Cerretti, Douglas P.
APPLICANT: BORGES, Luis G.
APPLICANT: BORGES, LUIS G.
APPLICANT: FAIRLOW, III, William C.
TITLE OF INVENTION: TEK ANTAGONISTS
FILE REFERENCE: 2900-A
CURRENT APPLICATION NUMBER: US/09/733,764
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 09/590,656
PRIOR FILING DATE: 1999-06-07
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                 LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-846-6
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US-09-499-846-6
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Best Local S
Matches 240
                                                                                                         Query Match 36.2%; Score 1235.5; DB 4; Best Local Similarity 66.2%; Pred. No. 6.3e-90; Matches 255; Conservative 18; Mismatches 54;
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SEQ ID NO 2
LENGTH: 704
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                                  GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN
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                                                                     GSGNLTLALEAKTGKLHQ---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE--
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 -NKEAKVSKREKPVWVLN---
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Pred. No. 7.9e-90;
9; Mismatches 12
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-- PEAGMWQCLLSDSGQVLLESNIK 385
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GENERAL INFORMATION:
APPLICANT: KAVANAUGH et al.
APPLICANT: KAVANAUGH et al.
TITLE OF INVENTION: FIEROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEO ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-499-846-4
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Best Local Similarity
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VFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                          VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                     LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
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                                                                                                                                                                                                                                                                                                                    GSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHS---
                                                                                                                                                                                                                                                                                                                                                   -----PEAGMWQCLLSDSGQVLLESNIK 385
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                                                                                  QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                    VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
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                                                   QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                                                                                                                                                                                ---PVPCPAP-----EPKSCDKTHTC----PELLGGPSVF
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/220
FILING DATE: 28-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr. James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cyto
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
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APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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 SVMHEALHNHYTQKSLSLSPG
                    SVMHEALHNHYTQKSLSLSPG
                                                              TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
                                                                                           TCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSC
                                                                                                                               LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
                                                                                                                                              LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSL
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Pred. No. 8.6e-90;
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RESULT 63
US-08-157-101A-7
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Sequence 7, Application US/08157101A Patent No. 5808032 GENERAL INFORMATION:
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Best Local Similarity 88.9%;
Matches 232; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Haley Jr, James F
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: Cyto
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 28-MAR-1994
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APPLICANT: Nocka, Karl (US only)
APPLICANT: Lobell, Robert B (US only)
TITLE OF INVENTION: STABILIZED DIMER OF
TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
NUMBER OF SEQUENCES: 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: United States
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51 Avenue of the Americas
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STRANDEDNESS: 6
7 TOPOLOGY: lines
7 MOLECULE TYPE: ps
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Best Local :
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9
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APPLICANT: MATSUKURA, SHIGEKAS
APPLICANT: TSURUOKA, NOBUO
APPLICANT: ARIMA, KENJI
APPLICANT: NISHIHARA, TATSURO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3711
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n 36.1%; Score 1232.5; DB 1; Similarity 46.7%; Pred. No. 9.7e-90; 7.7e-90; 41; Mismatches 91;
                         CLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPP 424
                                                                                                                                                                                                                                                                              HRFDSWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGG-TAALGCL
                                                                                                                                                                                                                                                                                                                                                   GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNKVVLGKKGDTVELTCTAS--QKKSIQFHW-----KNSNQIKIL---GNQGSFL--TK 71
                                                                                                   QEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQ
                                                                                                                                                                         SWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLH 309
                                                                                                                                                                                                           -----WNSGALASG- 178
                                                                                                                                                                                                                                              QKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSK 249
                                                                                                                                                                                                                                                                                                               HLLQ--GQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQN 189
                                                                                                                                                                                                                                                                                                                                                                                                                        GGGVV--QPGRSLRLSCAASGFTFSSNSMHWVRQAPGKGLEWVAVILYDGNHKFYADSVK 74
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MATSUKURA, SHIGEKAZU
TSURUOKA, NOBUO
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                                                                                                                                      -----VH-TFPAVL-QSSGLYSLSSVVTVPSSSLG 206
 EPKSCDKTHTCPPCPAPELLGGPSVFLFPP
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                                                                   -NHKPSNTKVDKKV---
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US-08-397-411-7
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                                                                                                                                                                                                                      ; MOLECULE TYPE: peptide US-08-397-411-7
                                                                                                                              Query Match 36.0%; Score 1230.5; DB 3; Length 446; Best Local Similarity 46.7%; Pred. No. 1.3e-89; Matches 284; Conservative 36; Mismatches 103; Indels 185; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-004901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08397411
Patent No. 6129914
                                                                                                                                                                                                                                                                                                       TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 446 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: T80, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 415-326-2400
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ADDRESSEE: Townsend
                                                                                                                                                                                                                                                              TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
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                                             LVKPSETLSLTCTVSGFSLTNYGVHWVRQSPGKGLEWIGVKWSGGSTEYNAAFISRLTIS 70
                                                                                 LGKKGDTVELTCTASQKKSIQF--HWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSL-
--WDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTLT 142
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One Market Plaza, Steuart Tower, Suite 2000
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USE S S S S S S S S S S S S S S S S S S	3 8	유 성	유 성	음 성	8	B 8	뭥	Ş	8 8	망	8	문
438 KSLSI ULT 65 -08-776-511-2 sequence 2, Appli satent No. 615315	μ	558 3,78	498 318	438 258	383 215	199	, o	. 263	203 145	114	143	71
XSISIS Applic ORMATI ORMATI ORMATI ORMATI ORMATI ORMATI ORMATI ORMATI INVENT IN	KSLSLSPG 62	8 VEWESNOOPENNYKTTPPVLDSDGSFFLYSKLTYDKSRWQQGNVFSCSVMHEALHNHYTQ 617 	8 YKCKVSNKALPAPIEKTISKAKGQPREPQVYT 	VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRIVSVLTVLHQDWLNGKE 49 	3 NIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPKFKDTLMISRTPE 437	QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKKEKFVWVLE : : CNVNHKPSNTKVDKKV		3 VKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQL 322	3 AFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELMWQAERASSSKSWITFULKNKEVS 2625	: : :	LESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVL 20	1 KDTSKNOVSLKINSLTAADTAVYYC

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GENERAL INFORMATION:
APPLICANT: KAVANAUGH et al.
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUS
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
CURRENT FILING DATE: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 488
TYPE: PRT
ORGANISM: Homo Bapiens
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US-09-499-846-12
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                                                                                                                                       US-09-499-846-12
                                                                                     Query Match
Best Local
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Best Local :
                                                                     Matches
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LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                               293 GSGNLTLALEAKTGKLHQ---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE-- 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 KLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHINEVVLLDAP 148
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                                                                                     Similarity
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GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TG---KLHQEVNLVVMR-----ATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK 356
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                                                                   Conservative
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Pred. No. 3.8e
36; Mismatches
                                                                 Score 1225; DB 4;
Pred. No. 4.2e-89;
8; Mismatches 56;
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                                                                                                                                                                                                                                                                                                            FUSION
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                                                                                                 Length 488;
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US-08-227-496C-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6130202
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15, Application US/08227496C Patent No. 6130202
                                                                                TELEFAX: (203) 812-549
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                     APPLICATION NUMBER: 07/903
FILING DATE: 06/22/92
APPLICATION NUMBER: 07/704
FILING DATE: 05/24/91
APPLICATION NUMBER: 07/556
FILING DATE: 07/20/90
ATTORNEY/AGENT INFORMATION:
                                                                                                                                  REFERENCE/DOCKET NUMBER: MT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Greve, Jeffrey M. APPLICANT: McClelland, Alan TITLE OF INVENTION: Multimeric TITLE OF INVENTION: Rhinovirus
                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 8.0 for Windows CURRENT APPLICATION DATA:
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MEDIUM TYPE: diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: C
DESCRIPTION:
                                TOPOLOGY:
                                                                LENGTH:
                                                                                                                                                                                    NAME: Barbara A. Shimei REGISTRATION NUMBER: 29,862
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                              : 680 amino acid residues amino acids
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protein
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Receptor Protein
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RESULT 68
US-07-934-373C-22
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                                                                                                                                                                                                                         Sequence 22, Application Patent No. 5821337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: LICAM(185
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                  STREET: 1 DNA way
CITY: South San Francisco
STATE: California
                                                                   COUNTRY:
                                                                                                                           ADDRESSEE:
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                                                                      USA
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DRMATION: amino acid residues 1-453 =
DRMATION: LICAM(453); amino acid residues 454-680 =
DRMATION: acid residues 216-442 of human IgG1 heavy
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                                                                                                                          Genentech, Inc
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                 445
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                 QKSLSLSPG
                                           QKSLSLSPG 625
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FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P070
TELECOMMUNICATION INFORMATION:
TELECHONE: 650/225-1994
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
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                                  AVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
                                                                                                                                EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDI
                                                                                                                                                                             EYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDI
                                                                                                                                                                                                                                                                    EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                                                                                                                                                                       EVTCVVVDVSHEDÞEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                              SNIKVLPTWSTPVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLE
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AVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS
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46.8%; Pred. No. 5.9e-89;
rative 35; Mismatches 110;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/71
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/L
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
                                                                                                                                                                                                                                                                                                                             Local Similarity
hes 285; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 40,378 REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/437,642B FILING DATE: 09-May-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Californi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/934373
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                                    153
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262 SVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQ 321
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                                                                                                                                                                                                                                                                                         LGKKGDTVELTCTASOKKSIOF--HWKNSNQIKILGNQGSFLTK-GPSKLNDRADSRRSL 86
                                                                      LAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEV 261
                                                                                                            TVSSASTKGPSVFPLAPSSKSTSGG-TAALGCL------
                                                                                                                                            TLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVV 201
                                                                                                                                                                                                                   ---WDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQ--GQSLTL 141
                                                                                                                                                                                                                                                       LVKPGASVKISCKTSGYTFTEYTMHWMKQSHGKSLEWIGGFNPKNGGSSHNQRFMDKATL
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                                                                                                                                                                                                                                                                                                                             35.8%; Score 1222.5; DB 3; Length 454;
46.8%; Pred. No. 5.9e-89;
wative 35; Mismatches 110; Indels 179;
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                                    VKDYFPEPVTVS-----
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                                    WNSGALTSG--
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US-08-146-206C-22
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                                                                     US-08-146-206C-22
Query Match 35.8%;
Best Local Similarity 46.8%;
Matches 285; Conservative 3
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APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                CLASSIFICATION: 530
PRIOR APPLICATION DATA:
RAPPLICATION UNMBER: 07/715272
RILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
                                                                                                                                       TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                         LENGTH: 459 .....
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/146,206C FILING DATE: 17-No. 6407213-1993 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGK 496
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                                                                                                                         454 amino acids
                                                                                                                                                                            650/225-1994
650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.5 inch, 1.44 Mb floppy disk
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; Score 1222.5; DB 4;
; Pred. No. 5.9e-89;
35; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTP 264
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   Indels 179;
                                  Length
                                  454;
 Gaps
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RESULT 71
US-09-705-686-22
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Patent No. 6639055
GENERAL INFORMATION:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-No. 6639055-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                 Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Carter, Paul J.
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STREET: 1 DNA Way
CITY: South San Francis
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                Inc
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 Sequence 22, Application PC/TUS9307832 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: Amino Acid
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   Immunoglobulin Variants
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/076
FILING DATE: 19930820
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REFERENCE/DOCKET NUMBER: 70
TELECOMMUNICATION INFORMATION:
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CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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FILING DATE: 21-AUG-1992
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Similarity 46.8%;
                              SNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTP 436
                                                                                                                                                                   SVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQ
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                                                                                               LQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLE
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460 Point San Bruno
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US-09-740-002-25
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Patent No. 6537809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR T
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BRAMS, APPLICANT: MORRO
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                                                                                                                                                                                                                              LSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFT 228
                                                                                                                                                                                                                                                                                                                                                            NSNQIKILGN-----QGSFLTKGPSKLNDRADSRRSLWDQGNFPLIKNLKIEDSDTYIC 109
                                                                                                                                                                                                                                                                                                                                                                                            LLLVLQLALLPAATQGNKVVLGKKGDTVELTCTAS-------
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                              AKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTH 408
                                                                                                                                                                                                 AALGCL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYT
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                                                                                             PQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKE 348
                                                                                                                                VS-----WNSGALTSG----
                                                                                                                                                                VEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQAL
                                                                                                                                                                                                                                                                                                                            -----QVVLSLTNVDPVDTATYYC 116
                                                                -QSSGLYSLSSVVTVPSSSLGTQTYI---
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 --NHKP-
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                                                   US-09-049-672A-4
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Query Match
Best Local Similarity
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                               IMMEDIATE SOURCE:
LIBRARY: PANCT
CLONE: 1513264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                            NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
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CITY: Palo Alto
                                                                                                                     TOPOLOGY:
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1221.5; DB
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                                                                                                                                                                                                                                                                                                                                              206 YSLSSVVTVPSSSLGTQTYI-----CNV-----CNV-----NHKPSNTKV
                                                                                                                                                                                                                                                                                                                                                                              295 GNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKR
                                                                                                                                                                                                                                                                                                                                                                                                                  184 -----WNSGALTSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 KEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 KILGNO--GSFLTKGPSKLNDRADSRRSL---WDQGNFPLIIKNLKIEDSDTYICEVEDQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 RHILLVIQLALLP-----AATQGNKVVLGKKGDTVELTCTAS--QKKSIQFHWKNSNQI
TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                          TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                  LPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                  LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                      PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                                                        PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
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US-08-470-299-4
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 75
                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08470299
Patent No. 5783181
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                    APPLICANT: Shatzman, All TITLE OF INVENTION: NO. NUMBER OF SEQUENCES: 21
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
                                                                                                           COUNTRY:
                                                                                             19406
                                                                                                                                       F: 709 Swedeland
King of Prussia
                                                                                                                       Pennsylvania
                                                                                                           USA
                                                                                                                                                                                                                                                 Chapman, Conrad
Clinkenbeard, H
Young, Peter R.
                                                                                                                                                                                                                                                                                              Murphy,
                                                                                                                                                                                                                                                                                                            Browne,
                                                                                                                                                                                                                                                                                              Kay E.
                                                                                                                                                                                                                                                                                                              Michael J.
                                                                                                                                                                                                                                                                                 Conrad G.
                                                                                                                                                                                                                    Allan R.
No. 5783181el Compounds
                                                                                                                                                        Beecham Corporation Road, P.O. Box 1539
                                                                                                                                                                                                                                                                 Helen
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                 Version #1.30
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APPLICANT: COSMAN, David J.
APPLICANT: MULLBERG, Jurgen H.
APPLICANT: MULLBERG, Jurgen H.
APPLICANT: MUSLOW III, William C.
APPLICANT: KUBIN, Marek
TITLE OF INVENTION: ULBP DNA AND POLYPEPTIDES
FILE REFERENCE: 2866-USA
CURRENT APPLICATION NUMBER: US/09/532,856
CURRENT FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: PCT/US98/27048
EARLIER FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: 60/069,857
EARLIER APPLICATION NUMBER: 60/092,946
EARLIER APPLICATION NUMBER: 60/092,946
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 10
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US-09-532-856-6
                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09532856 Patent No. 6458350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.7%; Score 1220.5; DB 1; Length 387; Best Local Similarity 83.4%; Pred. No. 6.8e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 610-270-5090 INFORMATION FOR SEQ ID NO: 4:
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(223)
OTHER INFORMATION: ULBP-2 sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: SULTON, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P31005C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                    ENGTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
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TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQP 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKRLDRNLWGL---AGLNSCPVKEANOSTLENFLERLKTIMREKDSKCSSGTEPKSADKT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE
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TITLE OF INVENTION: ULBP DNA AND POLYPEPTIDES
FILE REFERENCE: 2866-US
CURRENT APPLICATION NUMBER: US/09/524,100C
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: PCT/US98/27048
PRIOR FILING DATE: 1998-12-17
PRIOR PFILING DATE: 1998-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-07-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1

SEQ ID NO 6 LENGTH: 453 TYPE: PRT

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(223)

ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Peptide

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; LOCATION: (224)..(453)
; OTHER INFORMATION: Human Ig Fc sequences
US-09-532-856-6
                                                                                                                            ; Sequence 6, Application US/09524100C
; Patent No. 6653447
GENERAL INFORMÁTION:
APPLICANT: COSMAN, David J.
APPLICANT: MULLBERG, Jurgen H.
APPLICANT: FANSIOW III, William
APPLICANT: KUBIN, Marek
APPLICANT: KUBIN, Marek
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 NLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSP-KLMLSLKLENKEAKVSK- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 GELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 GPRWCAVQGQVDEKTFLHYDCGNKTVT-----PVSPLGKKL---
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                                                                                                                                                                                                                                                                                                                                                         VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
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                                            MULLBERG, Jurgen H. FANSLOW III, William C.
                                                                                                                                                                                                                                                  HEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Mismatches
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TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FU:
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF EG ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 497
TYPE: PRT
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US-09-499-846-10
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Best Local S
Matches 253
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Matches
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Patent No. 6656728
GENERAL INFORMATION:
APPLICANT: Kavanaugh et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Human 09-524-100C-6
                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: PEPTIDE LOCATION: (224)..
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                                                                                                         y Match: 35.7%;
Local Similarity 65.7%;
hes 253; Conservative 1
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108 258; Conservative
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                                               GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN
                                                                            GSGNLTLALEAKTGKLHQ---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEALHNHYTOKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTV
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58.9%;
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--NKEAKVSKREKPVWVLN------PEAGMWQCLLSDSGQVLLESNIK 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   452
                                                                                                         Score 1220.5; DB 4;
Pred. No. 9.8e-89;
.8; Mismatches 56;
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Pred. No. 8.6e-89;
1; Mismatches 70;
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VFSCSVMHEALHNHYTQKSLSLSPG

625 524

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Sequence 8, Application US/09499846
Patent NO. 6656728
GENERAL INFORMATION:
APPLICANT: Kavanaugh et al.
TITLE OF INVENTION: FIEROBLAST GROWTH FACTOR
TITLE OF INVENTION: RECEPTOR-IMMUNOGLOBULIN FUI
FILE REFERENCE: 035784/195012 (5784-
CURRENT APPLICATION NUMBER: US/09/499,846
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 8
LENGTH: 525
TYPE: PRT
ORGANISH: Homo Sapiens
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US-09-499-846-8
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Best Local Similarity
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                                                                                                                                                                                      263 ---AWLTVLEALEERPAVMTSPLYLEGSGSPGLOEPKSCOKTHTCPPCPAPELEGGPSVF
                                                                                                                                                                                                                      386 VLPTWST--
                                                                                                                                                                                                                                                     206 GSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHS---
                                                                                                                                                                                                                                                                                                               146 GSINHTYQLDVVERSPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVN
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                                                                               VVSVLTVLHQDMLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                                                            GSGNLTLALEAKTGKLHO---EVNLVVMRATQLQKNL--TCEVWGPTSPKLMLSLKLE--
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                                          LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                                                -----PEAGMWQCLLSDSGQVLLESNIK 385
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                                                                VVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                             LEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYNSTYR
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Pred. No. 1.1e-88;
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RESULT 81
US-09-301-593-18
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APPLICANT: Bevilacqua, Michael P.
APPLICANT: Bevilacqua, Michael P.
APPLICANT: Collins, David S.
TITLE OF INVENTION: COMPOSITION AND METHOD FOR TITLE REFERENCE: A-365F
FILE REFERENCE: A-365F
CURRENT APPLICATION NUMBER: US/09/131,247
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/055,185
EARLIER APPLICATION NUMBER: PCT/US 97/02131
EARLIER FILING DATE: 1997-08-08
EARLIER FILING DATE: 1997-02-10
NUMBER: OF SEQ ID NOS: 16
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US-09-131-247-16
Sequence 18, Application US/09301593A
Patent NO. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Leger, Olivier
APPLICANT: Sadanha, Jose W.
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SEQ ID NO 16
LENGTH: 388
TYPE: PRT
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GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEA--GMWQC 370
                                                                                                                                                                                                                                                                                            GNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                          KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPLFPEKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNST 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAMEADQPVSLTN---MPDEGVMVTKFYFQEDEAAAEPKSSDKTHTCPPCPAPELLGGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSDSGQVLLESNIKVLPTWSTPVPC-----PAPEPKSCDKTHTC----PELLGGPS 418
                                                                                                                                                                                                                                                                        GNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQ
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65.9%;
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Pred. No. 7.5e-89;
3; Mismatches 73;
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; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-04-30
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
                                                                                                                       RESULT 82
US-09-740-002-27
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Sequence 27, Application US/09740002
Patent No. 6537809
GENERAL INFORMATION:
APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: BUTTRALIZING HI
TITLE OF INVENTION: SPECIFIC TO RS
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Matches 281; Conserv
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                                                                                                                                                                                                              QKSLSLSPG
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46.1%; Pred. No: 1e-88;
vative 42; Mismatches 107;
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HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES RSV F-PROTEIN AND METHODS FOR THEIR

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RESULT 83
US-08-487-550-12
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                            Sequence 12, Application Patent No. 6113898 GENERAL INFORMATION: APPLICANT: Anderson,
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LENGTH: 475
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Best Local :
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CURRENT APPLICATION NUMBER: U99/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
 TITLE OF INVENTION:
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45.0%;
, Darrell R.
"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FV
                                                                                 US/08487550
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Pred. No. 1.1e-88;
1; Mismatches 116;
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Best Local 9
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ZIP: 23114
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS LENGTH: 476 amino acids
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REFERENCE/DOCKET NUMBER: 012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: PH
TITLE OF INVENTION: IM
NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 69
CITY: Alex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
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                            590
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Similarity 53.7%;
77; Conservative 3:
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TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                      TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                             LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                              PREEQYNSTYRVVSVLTVLHQDWLNGKBYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
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Pred. No. 1.1e-88;
1; Mismatches 89;
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                                                                                                                                                                                                                                                                                             -NIKVLPTWSTPVPCPAPEPKSCDKTHTC----
 475
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acids
TYPE: amino acid
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US-09-526-098-12
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PATENT NO. 6492134

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 277; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10707071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
FILING DATE:
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
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                                                                            142
                                                                                                                  334
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                                                                                                                                                                                      281 HLTLPQALPQYAGSGNLTLALEA----KTGKLHQEVNLVVMRATQLQKNLTCEVWGP--- 333
                                                                                                                                                                                                                                                                                                                                             171 VSQLELQDSG-----TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVE 220
202 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPS-NTKVDKKA-EPKSCDKTHTCPPCP 259
                                                                                                                                                                                                                                                                   221 FSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPL 280
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                                                                                                                                                                                                                                                                                                             LSQVQLQESGPGLVKPSETLSLTCAV-----
                                    LLSDSGQVLLES----- 410
                                                                          VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 201
                                                                                                              -----TSPKLMLSLKLENKEAKVSKR------EKPVWV-----LNPEAGMWQC 370
                                                                                                                                                    -----NNWFDVWGPGVL 141
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ilarity 53.7%;
Conservative 3
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Pred. No. 1.1e-88;
1; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                      Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 476;
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426 PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 485	6	^
187 VLQSSGLYSLSSVVTVPSSSDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPK 241	87	_
371 LLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVFLFPPK 425	71	_
latch 35.6%; Score 1216; DB 4; Length 442; cal Similarity 89.6%; Pred. No. 1.9e-88; conservative 3; Mismatches 14; Indels 10; Gaps 2;	Query Match Best Local Similarity Matches 233; Conser	
ATION FOR SEQ ID NO: 7: ENCE CHARACTERISTICS: NGTH: 442 amino acids PE: amino acid PE: unknown POLOGY: linear CULE TYPE: protein -888A-7	8 7 A A G T 9	d
REGISTRATION NUMBER: 35,238 REGISTRATION NUMBER: 35,238 REFERENCE/DOCKET NUMBER: 00786/258001 LECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200 TELEFAX: 617-428-7045 TELEX:	REGISTRATION N REFERENCE/DOCK REFERENCE/DOCK TELECOMMUNICATIO TELEPAN: 617- TELEX:	
ON DATA: UMBER: 23-NOV- INFORMAT	PRIOR APPLICATI APPLICATION N FILING DATE ATTORNEY/AGENT NAME:	
**************************************	CURRENT APPLICATION APPLICATION FILING DATE: CLASSIFICATION	
OZALIO READABLE FORM: TYPE: Diskette ER: IBM Compatible ING SYSTEM: DOS	COMPUTER READA COMPUTER READA COMPUTER: I COMPUTER: I COMPUTER: I COMPUTER: I COMPUTER: I	
176 176 Seton	170 170 170	
LICANT: Seed, BITAN LICANT: WAIZ, GETE B OF INVENTION: AGP-ANTIBODY FUSION PROTEINS LE OF INVENTION: AND RELATED MOLECULES AND METHODS LES OF SEQUENCES: 9 LESPONDENCE ADDRESS:	APPLICANT: Se APPLICANT: We APPLICANT: We ITITLE OF INVEN ITITLE OF SEQU CORRESPONDENCE	
88A-7 7, Applicati . 6613746 . IFORMATION	RESULT 85 US-08-472-888A-7 ; Sequence 7, Appli ; Patent No. 661374 ; GENERAL INFORMAT ; GENERAL TOWN.	
590 TVDKSRWQQGNVFSCSVMHBALHNHYTQKSLSLSPG 625	90 40	
530 LPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 589 		
470 PREEQVNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT 529 		
411 -PELLGGPSVFLFPPKPKDTLMISRTPBVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 469		

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PCT-US96-10043-9
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GENERAL INFORMATION:
APPLICANT: The General Hospital C
                                                                                                                                                                                           Best
                                                                                                                                                                                                               Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COFFRATING SYSTEM: PC-DOS/MS-DOS
COFFRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
TITLE OF INVENTION: AND METHODS
                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Lech, Karen F.
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APPLICATION NUMBER:
FILING DATE: 14-JUN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                               Local 233;
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CITY: Boston
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                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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486
                                                                                                                                         371 LLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPK 425
                                                                                                                                                                                            Similarity
                                                                                                        VLOSSGLYSLSSVVTVPSSSDKKV-----EPKSCDKTHTCPPCPAPELLGGPSVFLFPPK
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TVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLT 545
                                                     PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
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                                  PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL
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225 Franklin Street
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                                                                                                                                                                                           Score 1216; DB 5;
Pred. No. 1.9e-88;
                                                                                                                                                                            ed. No. 1.9e-88;
Mismatches 14
                                                                                                                                                                                                               Length 442;
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PCT-US96-10043-11
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                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
FILING DATE: 14-UN-1995
CLASSIFICIATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: P-SELECTIN TITLE OF INVENTION: AND METHODS NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02210-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                    397 PAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
323
                                                                                  452 VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                 203 PEGEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE
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                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                               VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VMHEALHNHYTOKSLSLSPG 441
 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK
                   EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 571
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                                                                                                                                                                                                                                                                                                                                                  437 amino acids
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                                                                                                                                                                                                                                                                                                                 not relevant
                                                                                                                                                                                                                  35.6%;
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Pred. No. 2e-88;
O; Mismatches
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RESULT 89
US-09-157-452B-12
; Sequence 12, Application US/09157452B
; Patent No. 6482409
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US-08-378-939-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/952640
FILING DATE: 01-DEC-1992
ATTORNEY/ACENT INFORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (202) 783-6031
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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No. 5876967
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Y: U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                      PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                      ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 574
                                                                                                                                                                                                                             NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                      NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 514
                                                                                                                                                                                                                                                                                                                    EPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 454
                                                                                                                                                             ISKAKGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTP
                                                                                               PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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555 THIRTEENTH ST. N.W.
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Pred. No. 2.5e-88;
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                                                                                                                                                                                                                                                                                                                                                                                   Length 476;
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APPLICANT: LOBD, ROY R.
APPLICANT: BURKLY, Linda C.
FILE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 10274-004003
CURRENT APPLICATION NUMBER: US/09/157,452B
CURRENT PILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: US 08/950,660
PRIOR FILING DATE: 1997-10-15
PRIOR APPLICATION NUMBER: US 08/933,857
PRIOR APPLICATION NUMBER: US 08/373,857
PRIOR FILING DATE: 1997-01-18
PRIOR APPLICATION NUMBER: US 08/284,603
PRIOR APPLICATION NUMBER: US 07/835,139
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
TENCTH: 446
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 TANSDTHLLQ-GQSLTLTLESPPGSSP----SVQCRSP-RGKNIQGG--KTLSVSQLELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 NEHSYLCTATCESRKLE-------KGIQVEIYSFP------
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                                                                                                                                                                                          REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
                                                                                                                                                                                                                                                                          PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKF
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VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                            VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                            PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                                  REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
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                                                                                PPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLT
                                                                                                                                                                                                                                                    PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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52.4%; Pred. No. 3e-88;
tive 40; Mismatches
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; Sequence 13, Application U
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sun
; APPLICANT: Tso, J. Yun

US/08458516

Co, Man Tso, J.

RESULT 90 US-08-458-516-13

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RESULT 91
US-09-485-737B-67
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                                                                                                                                                                                  Sequence 67, Application US/09485737B Patent No. 6350860
                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
FILE REFERENCE: INNS:015
FULE REPERENCE: INNS:015
CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-326-2422 INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/0:
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: William M. Smith STREET: One Market Plaza, Storry: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                 PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                           PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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97.8%;
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Pred. No. 3.3e-88;
0; Mismatches 0;
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RESULT 92
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 67
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Best Local Similarity
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR FILING DATE: 1997-08-18
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                    472
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45.3%;
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Pred. No. 3.96
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1.9e-88;
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GENERAL INFORMATION:
APPLICANT: Buyse, Marie-Ange
APPLICANT: Sablon, Erwin
TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS

REFERENCE: INNS:015

Sequence 90, Application US/09485737B Patent No. 6350860

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CURRENT APPLICATION NUMBER: US/09/485,737B
CURRENT FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: PCT/EP 98/05165
PRIOR FILING DATE: 1998-08-14
PRIOR APPLICATION NUMBER: EPO 98870139.7
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: EPO 97870122.5
PRIOR PILING DATE: 1997-08-18
NUMBER OF SEQ ID NOS: 104
SOPTWARE: PRICENTIN VERBION 3.0
SEQ ID NO 90
LENGTH: 711
RESULT 93
US-09-313-942-7
; Sequence 7, Application US/09313942
; Patent No. 6472179
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RV--
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                                                                                                                                                                DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                       EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKGQPREPQVYTLP 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC-----P 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSSVVTVPSSSLGTQTYI------CNV-----CNV-----NHKPSNTKVDK 233
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APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AN
TITLE OF INVENTION: AND USING
FILE REFERENCE: REG 203-A
CURRENT APPLICATION NUMBER: US/09/313,942
CURRENT FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 09/313,942
PRIOR FILING DATE: 1999-05-19
PRIOR APPLICATION NUMBER: 00/101,858
PRIOR APPLICATION NUMBER: 60/101,858
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
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                                                                                                                                   ; TYPE: PRT
; ORGANISM: Homo
US-09-313-942-9
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US-09-313-942-9
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-313-942-7
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                                                                 Query Match
Best Local Sin
Matches 226;
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09313942 Patent No. 6472179
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Best Local Similarity
Matches 229; Conserv
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                                                                                                                                                                                    LENGTH: 951
                 400 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 454
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EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                                                   Conservative .
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                                                               Score 1212.5; DB 4; Pred. No. 1.1e-87; 0; Mismatches 0;
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Pred. No. 9.3e-88;
3; Mismatches 5;
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RESULT 95
US-09-247-
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APPLICANT: Stadak, Anthony W.
APPLICANT: Stadak, Anthony W.
APPLICANT: Berry, Karen K.
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgen
APPLICANT: Huse, William D.
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; TYPE: PRT
; ORGANISM: Human and
US-09-247-352-3
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 35.5%; Score 1212; DB 4; Length 451; Best Local Similarity 46.7%; Pred. No. 4e-88;
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                                                                                                                                                                                                                                                                                                                                                                                              Matches
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TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN
FILE REFERENCE: DB2a SEQUENCE
CURRENT APPLICATION NUMBER: US/09/247,352
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 09/026,291
EARLIER FILING DATE: 1998-02-19
MUMBER: OF SEQ ID NOS: 14
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 VLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC----PELLGGPSVFLFPPKPKDTLMI 432
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                                                                       RATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQ 377
                                                                                                                               NKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVM
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GENERAL INFORMATION:
APPLICANT: Aruffo, Alejandro A.
APPLICANT: Siadak, Anthony W.
APPLICANT: Siadak, Anthony W.
APPLICANT: Harris, Linda
APPLICANT: Harris, Linda
APPLICANT: Thorne, Barbara A.
APPLICANT: Thorne, Barbara A.
APPLICANT: Bajorath, Jurgen
TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN CD4
FILE REFERENCE: DB2 SEQUENCE
CURRENT APPLICATION NUMBER: US/09/466,635
CURRENT FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 8
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 451
TYPE: PRT
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Best Local Similarity
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433 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 492
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46.7%; Pred. No. 4e-88;
7ative 34; Mismatches 103;
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                                                     -EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTL-I
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GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Saldanha, Jose W.
APPLICANT: Nettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT APPLICATION NUMBER: EP 98107925.4
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1999-04-30
EARLIER FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 30
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-30
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US-09-301-593-30
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Patent No. 6455677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 266;
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HEDPEVKFNMYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPVPCPAPEPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 446
                                                                                                                                                                      GPTSPKLMLSLKLENKEAKVSKREKPVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWS
                                                                                                                                                                                                                                              LTLPQALPQYA----GSGNLTLALEA-----KTGKLHQEVNLVVMRATQL-QKNLTCEVW 331
                                                                                                                                                                                                                                                                                                                    SFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLH 281
                                                                                                                                                                                                                                                                                                                                                                                                KTLSVSQLEL-----QDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEF 221
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                                                                                                                                   ----- NHKPSNTKVDKKV------ 240
                                                                                                                                                                                                                                                                                                                                                             KSSSTAYMELRSLTSEDSAVYFCA----RRRIAYGYD------EGHAMDY
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                                                          -EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 472;
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; MOLECULE TYPE:
US-08-595-043A-50
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local Similarity 97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: SGARLATO,
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION UNMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET,
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
                                                                                                 515 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 574
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 181
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o. 5935824
                                                                                                                                                                                                                            1 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
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                                     PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                          ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
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                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                Score 1211.5; DB 2;
Pred. No. 1.7e-88;
0; Mismatches 0;
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RESULT 99 US-09-178-869-2

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APPLICANT: Hamman, Joseph P.
TITLE OF INVENTION: CELL SUFFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/761,413
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/09/178,869
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOUTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 331
TYDE: PRT
ORGANISM: Homo sapiens
US-09-761-413-2
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GENERAL INFORMATION:
APPLICANT: Mong, Shou
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
APPLICANT: Hammang, Joseph P.
APPLICANT: Baetge, E. Edward
TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION
FILE REFERENCE: 17810-043
CURRENT APPLICATION NUMBER: US/09/178,869B
CURRENT FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-178-869-2
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US-09-761-413-2
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Patent No. 6506891
GENERAL INFORMATION:
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Best Local Similarity 97.8%;
Matches 226; Conservative
                                                                                      Query Match
Best Local Similarity
Matches 226; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tao, Weng
APPLICANT: Wong, Shou
APPLICANT: Hickey, William F
APPLICANT: Hammang, Desegh P.
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                       400 EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 454
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  100 EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 159
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                                                                                        Conservative
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Search completed: August 3, 2004, 13:17:11 Job time : 29.0695 secs

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which encode CD4 or a plasmid which encodes gene has been deleted
                                                           WPI; 1989-214472/30.
N-PSDB; AAN90357.
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                                                                                                                                                             Fusion protein;
diagnosis; CD4;
                                                                                                                                                                               upstream
                                                                                                                                                                                     Genetic
                                                                                                                                                                                                25-MAR-2003
02-NOV-1992
                                                                                                                                                                                                                  AAP93009;
                                                                                                                                                                                                                              AAP93009 standard;
                  The fusion protein
                             Example;
                                                                                                    22-JAN-1988;
                                                                                                                           26-JUL-1989
                                                                                                                                                 Homo sapiens
                                         Immunoglobulin-CD4 fusion proteins infections or detecting HIV or SIV
                                                                                                               20-JAN-1989;
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                                                                                                                                                                                                                                                                            GEN
                                                                                                                                                                              construct which encodes CD4 linked to human IgG1 at \mathfrak m of the hinge region (fusion protein CD4E-gamma-1).
                            Table 2, Page
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                                                                                                                                                             immunoglobulin-like molecule; HIV; SIV; therapy;
gp120; binding fragment; glycoprotein; variable region
genes of the invention pref. comprise cDNA sequences ra fragment which binds gpl10 ligated to an expression des an antibody in which the variable region of the ted (see WO87-02671). The CD4 portion of the fusion
                                                                                                                                                                                                                              protein;
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Human CD4

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gp120; therapy;

diagnosis.

CD4; IgG1; human; CD4Egamma1; fusion protein; immunoglobulin; HIV; SIV;

RESULT 2
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entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 631 AA;
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                                                                                                                                                                                                                                            LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEEPKSCDKTHTCPPCPAPELLG
                                                                                                                                                                                                                                                                                                                          LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                    QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                 WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                         ELTKNOVSLTCLVKGFY
                                                                         ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                    NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                      NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                                                                                 GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                                                                                 GPSVELFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKFREEQY
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                                                                                                                                                                                                                                                                                                       LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
WQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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                                                           PSDIAVEWESNGQPENN
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                                                              KTTPPVLDSDGSFFLYSKLTVDKSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Protein
                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example
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619; Conserv
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                                                                                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                          QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                        QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                           Conservative
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
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Pred. No. 3e-166;
0; Mismatches
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This invention describes a novel nucleic acid (I) encoding a fusi protein comprising a DNA sequence encoding amino acids 1-173 of C and a DNA sequence encoding a human immunoglobulin (Ig) heavy or chain (III). The products pf the invention have anti-human immunodeficiency virus. (HIV) activity and are capable of binding gp120. The fusion protein is useful for treating human immunodeficiency virus (SIV). This sequence virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from linked to human IgG1 upstream of the hinge region

human immunodeficiency This sequence

from CD4

of CD4

(II)

or light

Example

1; Col

29-42; 39pp; English

Sequence 631

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23-JAN-1989;
09-JUN-1992;
                                                                                                                Fusion protein useful
                                                                                                                                                           Seed
                                                                                                                                                                                                                                                                                   Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                   04-FEB-1994;
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                                                                                                                                                                                                                                                                                                                                    Human
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89US-00299596.
92US-00896781.
93US-00057952.
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RESULT 4
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ID AAYS9
XX AAYS
AC AAYS
XX AAYS
XX HIV,
XX HIV,
XX HEQ;
XX Synt
OS Homc
XX CAL:
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XX PR 20-{
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Best Local Similarity
Matches 619; Conserv
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Pred. No. 3e-166;
0; Mismatches
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Best Local S
.Matches 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gpl20 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gpl20 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CD4Egammal where the CD4 is linked to human IgG1 at the Esp site upstream of the hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1;
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DB; AAZ48202.
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                                                                                                                                                                                                                                                                                                                             QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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   ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                   ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                              NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
                                                                                                                          GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
                                                                                                                                         GPSVFLFPPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
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ilarity 98.3%;
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Matches 621; Conserv
                                                                                                                                                                                                                                                        The fusion protein genes of the invention pref. comprise cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see w087-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The 19 heavy chain is pref. from IgM, IgG1 or IgG3. The following are specifically claimed: fusion proteins CD4H-gamma-1, CD4Hmu, CD4E-gamma1, and CD4Hmu (NO.67608), pCD4P-gamma (NO.67609) and pCD4E-gamma1 (NO.67609) at pcb4: GD4Hmu (NO.67608) at the ATCC under accession number 67611. (Updated on 55-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetic construct which encodes site upstream of the CH1 region
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N-PSDB; AAN90356.
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02-NOV-1992
                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunoglobulin-CD4 fusion proteins - used for infections or detecting HIV or SIV in sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                          | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                   729
                                                                                                                                                                                                                                                                                                                                                                                                                                Table 1,
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TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                        LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin-like molecule; HIV; SIV; therapy;
gp120; binding fragment; glycoprotein; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                               Page 12-23; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                           93.0%;
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Pred. No. 2.5e.
0; Mismatches
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protein CD4H-gamma-1).
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                                          23-JAN-1989;
09-JUN-1992;
12-APR-1993;
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gp120;
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                          04-FEB-1994
                                                                                                               22-JAN-1988
                                                                                                                                                                                                       12-SEP-2000
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0; therapy; di
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                     88US-00147351.

89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
                                                                                                                                                          95US-00479353
                                                                                                                                                                                                                                                                                                                      400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein CH4Hgammal.
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         /note= "CD4 extracellular region"
                                                                                                                                                                                                                                                                                                 note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4Hgamma1; fusion
                                                                                                                                                                                                                                                                       .729
.e= "IgG1 heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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Query Match
Best Local S
Matches 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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N-PSDB; AAA50660.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
YKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIA
                                                                                                                                                                                                                                  TAALGCLVVSYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                                                                                                                                                                                                                                                                                                                                                                         LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                               LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                           VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                        VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                         ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                              LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
                                                                                                                                                                                                                                                                                                                                                                                                                     LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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0; Mismatches 4;
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                         Query Match
Best Local (
                                                                                                                                                                               The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which caused for treating HIV or SIV infections in humans. The present sequence represents the fusion protein in the fusion protein in the fusion protein in humans. The present sequence represents the fusion protein CD4Hgammal where the CD4 is linked to human IgG1 at the Hind3 site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV; extracellular; CD4; gpl20; immunoglobulin; secreted protein; SIV infection; medicament.
                                                                                                      Sequence 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New fusion gene encoding immunoglobulin-CD4 fusion proteins, use the treatment of HIV or simian immunodeficiency virus infections
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                                                                                                                                                         upstream of the CH1
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Similarity 85.3%;
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23-JAN-1989;
09-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----PAP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                              immunodeficiency virus;
                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                      (first
88US-00147351.
89US-00299596.
92US-00896781.
93US-00057952.
                                                                                                       94US-00191708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          729
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                                                                                                                                                                                                                                                                                                                    immunoglobulin;
                                                                                                                                                                                                                                                                                                 CD4H-J
                                                                                                                                                                                                                                                                                                                  gp120;
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Query Match
Best Local S
Matches 620
                                                                                       This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding anino acids 1-173 of CD4 (II) and a DNA sequence encoding a mino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to 1912. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4H-1 which is constructed from CD4 linke to human IgG1 upstream of the CH1 region
                                                             Sequence
                                                                                                                                                                                                                                                                                   Fusion protein useful
                                                                                                                                                                                                                                                                                                                                                                                              (GEHO)
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DB; AAZ44061.
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92.8%;
nilarity 85.2%;
Conservative
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                                                                                                                                                                                                                                                    English
Score 3166.5; DB 3
Pred. No. 8.8e-163;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                   treatment
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                           Length
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Local Similarity
les 620; Conser
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                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                 MRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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VEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
                                                                                                VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                                                                                                                                                       LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPC------------
                                          YKCKVSNKALPAPI
                                                                               VTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKE
                                                                                                                                      ICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVPLFPPKPKDTLMISRTPE
                                                                                                                                                                                          TAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTY
                                                                                                                                                                                                                                              LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPEASTKGPSVFPLAPSSKSTSGG
                                                                                                                                                                                                                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                        EPKSCDKTHTC-----PELLGGPSVFLFPPKPKDTLMISRTPE
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RESULT 9
AAV5108
JD AAV55
XX AAV5
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XX AAV5
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similar immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Egammal which is constructed from CD4 linked to human IgG1 upstream of the hinge region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein; human; CD4; IgG1; immunoglobulin; anti-human immunodeficiency virus; CD4Bgamma1.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 616 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Col 59-70; 39pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human fusion protein CD4Bgammal.
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                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                              MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                                                                                                Conservative
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89US-00299596.
92US-00896781.
93US-00057952.
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                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                          Score 3163; DB 3;
Pred. No. 1.1e-162;
0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                           Length 616;
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N-PSDB; AAZ48205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD4-Ig fusion protein CD4Bgammal.
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The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which b to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA

which bi

binds

New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in the treatment of HIV or simian immunodeficiency virus infections.

Example 1;

Page 61-68; 89pp; English.

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RESULT 11
AAP93012
ID AAP93
XX
AAP93
XX
AC AAP93
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DT 25-M
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Best Local S
Matches 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gpl20 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein CD4Bgammal where the CD4 is linked to human IgG1 at the Banl site
                               Genetic
                                                                                                                                    AAP93012
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               construct which encodes CD4 linked to human IgG1 at the eam from the hinge region (fusion protein CD4Blambda1).
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                                                                                                                                                                                                                                                                      VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN 540
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(first entry)
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Fusion protein;
diagnosis; CD4;
                                                                                                      26-JUL-1989
                                                                                                                    sapiens
                                                                                                                           immunoglobulin-like molecule; HIV; SIV; therapy; gp120; binding fragment; glycoprotein; variable
                                                                                                                            region.
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Seed 22-JAN-1988; 20-JAN-1989; (GEHO) 1989-214472/30. DB; AAN90360. GEN HOSPITAL 88US-00147351 89EP-00100913 CORP

Immunoglobulin-CD4 fusion proteins infections or detecting HIV or SIV used for in sample. treating õ

Example; Table 5, Page 48-55; 68pp; English.

The fusion protein genes of the invention pref. comprises cDNA sequences which encode CD4 or a fragment which binds gp120 ligated to an expression plasmid which encodes an antibody in which the variable region of the gene has been deleted (see Wo87-02671). The CD4 portion of the fusion protein may comprise the complete CD4 sequence, the 370 AA extracellular region and the membrane spanning domain, or the extracellular region. The 19 heavy chain is pref. from My. IGG1 or IGG3. The following are specifically claimed: fusion proteins CD4Flambda1, CD4Fmu, CD4Fmu, CD4Elambda1, and CD4Mmu (No. 67608), pCD4Plambda (No. 67609) and pCD4Elambda1 (No. 67610). (Updated on 25-MAR-2003 to correct PA field:)

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                                                         LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                             The present sequence is that of fusion protein CD4Bgammal comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its C-terminus to the human IgG1 heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgG1 DNA at the Ban1 site downstream of the hinge region (see AAA50664). Fusion protein CD4Bgammal and a nucleic acid, end a method of producing the fusion protein avector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NNR imaging agent. The fusion protein the fusion protein such as CD4Bgammal provide both and tissue stains. IgG1 fusion proteins such as CD4Bgammal provide both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD4; IgG1; human; gp120; therapy; di
                                                                                                                                                                                                                                                                                                                                                                                        Example 1;
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303. .317
/label hinge
318. .427
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205. .302
/label= CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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Pred. No. 1e
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                                                                                                                                                                                                                                                expression vector; HIV;
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Best Local Similarity
Matches 457; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The human CD4 cDNA is excised from the plasmid pSP6T4 and cloned into M13mpl8. In order to excise a fragment containing the CH1 exon of the human gamma 1 heavy chain gene, the plasmid pBr gamma 1 is digested with SacII, and the SacII sites are then made flush using T4 DNA polymerase. The fragment containing the CH1 exon is then purified and ligated to the M13mpl8 (CD4) vector. Oligonucleoride-mediated site-directed mutagenesis is then performed to juxtapose the CD4 and CH1 sequences in frame. The CD4-CH1 chimeric gene is then linearized and ligated to the Pst1-Pst1 DNA fragment of the plasmid pBr gamma 1 containing the hinge, CH2, and CH3 exons of the human gamma 1 chain gene designated CD4-IgG1HC-pRcCMV (ATCC 75192). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4-gamma 1 chimeric heavy chain homo-dimer and its expression vector for preventing and treating HTV infection useful as a diagnostic agent
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                 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                  TLALEAKTGKLHQEVNLVVMRATQL-QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK 356
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72.1%;
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Pred. No. 1.9e-111;
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28-JAN-1993
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Human CD4 cDNA was excised from pSP6T4 and cloned into M13mp18. The 2 kt PstI/PstI fragment from pBR lambda 1 contg. the human lambda 1 heavy chain gene (contg. the hinge, CD2 and CH3 exons) was isolated and cloned into the BAP-treated M13mp18/CD4 vector. To obtain a CD4-lambda 1 chimeric heavy chain gene, oligonucleotide-mediated site-directed mutagenesis was performed to juxtapose the CD4 and lambda 1 heavy chain DNA sequences, ligating the CD4 sequence in frame to the hinge exon. The DNA was then cloned into pcDNA-1 to produce CD4-IgG1-pcDNA1 (ATCC 40951) (Updated on 25-MAR-2003 to correct PN field.)

cloned Š Example; Fig

w --

88pp; English.

Sequence 435

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RESULT 15
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DT 24-OC
DT 25-MA
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Best Local S
Matches 428
                                                                                                                                                                                         24-OCT-2003
25-MAR-2003
                                                                                                                     chimeric;
                                                                                                                                                        CD4-IgG2
                                                                                                                                                                                                                                                     AAR26783 standard; protein; 530
                        Domain
                                               Domain
                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302
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28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                        chimeric heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTC-----PELLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKI
                                                                                                                                                                                                                                                                                                                            QQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLL
                                                                                                                                                                                                                                                                                                                                                              LTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                          LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                                                                                                                             STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                          STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WTCTVLQNQKKVEFKIDIVVLAF-
                                                                                                                                                                                                                                                                                                              QQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EPKSCDKTHTCPPCPAPELLGG
                                                                                                                   increased
                                                                                                                   soluble CD4; T
increased serum
                                                                                                                                                                             (revised)
(revised)
(first entry)
206. .302
/label= CH1
303 .312
                       /label= CD4 domain
206. .302
                                                         Location/Qualifiers
                                               . 205
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half
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Pred. No. 1.2e-107;
0; Mismatches 1;
                                                                                                                     receptor;
life; HIV
                                                                                                                                                                                                                                                                                                                                      625
                                                                                                                                                                                                                                                                                                                434
                                                                                                                     CD4 antigen; high recovery; infection; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a CD4-IgG2 chimeric heavy chain heterotetramer It was produced by expresion of the coding mutagenised cDNA (produced as described in AAQ28089) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a heterotetramer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV cf. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas exoroxin A (domains) I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 15; Fig 4; 90pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors treatment, prevention and diagnosis of HIV infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9213947-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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      357
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                                                                                                                                                                                                                                                            121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                          al Similarity
437; Conserv
                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                             61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                          GA,
                                                                                                                                                                                               TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                             MNRGVPFRHLLIVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
        PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV-----
                                                                                                                                      QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG----SGNL
                                         TFPAVLOSSGLYSLSSVVTVPSSNFGTQTYTCNV
                                                                      TLALEAKTGKLHQEVNLVVMRATQL-QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
                                                                                                                                                                                                                                                                                                                                                                                                                                         62.0%;
ilarity 68.9%;
Conservative 2
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/label= CH3
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                                                                                                           ----PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2116; Di
Pred. No. 2.8e
25; Mismatches
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.8e-106;
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        PCPAPEPKSCDKTHTCP
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Gaps

240

297 216 180 120 120 60

-SNTKVDKTVERKCCVECPPCPAPP-

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This sequence represents the CD4-IgG2 chimeric heavy chain amino acid consequence from the CD4-IgG2 chimeric herotetramer. The invention relates to an immunoconjugate comprising a cytotoxic radionuclide and a cytotoxic radionuclide is linked to either the heavy chains or the light chains. The cytotoxic radionuclide is linked to either the heavy chains or the light chains, or consider the response are chimeric CD4-Ig (immunoglobulin) G2 chains encoded by cector CD4-IgG2HC-pRcCMV (ATCC 75193) and both light chains are chimeric CD4-IgG2HC-pRcCMV (ATCC 75193) and both light chains are chimeric CD4-kappa chains encoded by vector CD4-Kappa chai
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06-AUG-1993;
03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                 New immunoconjugate, used to treat, prevent or image human ideficiency virus infection, comprises radionuclide attached heterotetramer of CD4-immunoglobulin chimeras.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4-IgG2 chimeric heavy chain heterotetramer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging; prognosis; envelope glycoprotein burden; human.
                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-269502/23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric heterotetramer heavy chain amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
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93WO-US007422.
95US-00379516.
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RESULT
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DT 23
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CD CD

AAB67323

standard;

protein;

23-APR-2001

(first entry)

CD4-IgG2 chimeric heavy chain

protein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or preventing infection. It is also used for imaging HIV-infected tissues (for staging or prognosis of infection, and for assessing efficacy of treatments). The immunoconjugate is also used to determine the HIV envelope glycoprotein burden, once determined, this information is used in the staging and prognosis of HIV infected patients. The immunoconjugate should be active against all strains of HIV (since the CD4-gpl20 interaction is essential for infection). The heterotetramers are assembled intracellularly and secreted efficiently from mammalian cells, allowing high recovery and purification from the culture medium. They have longer half-life in serum and greater avidity than heavy chain
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                    DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                                         PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                               EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                            --VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                   PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTV
                                                                                                                                          EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                   P-----SNTKVDKTVERKCCVECPPCPAPP---
                                                                                                                                                                                                                                                                                                                    PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV-----PCPAPEPKSCDKTHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                             ------PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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; Pred. No. 2.86
25; Mismatches
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Matches 437
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06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterotetramer having two chimeric CD4-IgG2 heavy chains encoded by an expression vector CD4-IgG2HC-pRCCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-kLC-pRcMV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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kappalight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-
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ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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                                                                     PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----
                                                                                                  TFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNV-
                                                                                                                          TLALEAKTGKLHQEVNLVVMRATQL-QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
                                                                                                                                                                                  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---
                                                                                                                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAF--AST-----KGPSV---FPLA------
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93WO-US007422.
95US-00379516.
95US-00477460.
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Pred. No. 2.8e-106;
5; Mismatches 58;
                                                                                                                                                        --PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                           SNTKVDKTVERKCCVECPPCPAPP
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                                                                       PCPAPEPKSCDKTHTCP
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RESULT 18
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08-FEB-1991;
10-FEB-1992;
08-DEC-1992;
                                    The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2 chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IgC2HC-PRCCMV (VI) and CD4-KLC-PRCCMV (V2), respectively. The method is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+cells infected with HIV. The prevent CD4-IgG2 chimeric heterotetramer. This sequence was used in the
                                                                                                                                                                                                                                                               Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ or treating a subject having CD4+ cells infected with HIV involves CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
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                                                                                                                                                                                                                                     Disclosure; Fig
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                         the present invention
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92WO-US001143.
92US-00960440.
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Query Match Best Local (Matches

Similarity

62.0%;

Score Pred.

2116; DB 4; No. 2.8e-106;

Length 530; Indels

114;

Gaps

10;

Sequence

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ABG71123
ID ABG71123
XX ABG71123
XX ABG711
XX ABG71
XX ABG71
XX CD4-1
XX CD4-1
XX CD4-1
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                                                                              Protein
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26. .530
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SQ Sequence 530 AA;

Query Match
62.0%; Score 2116; DB 6; Length 530;
Best Local Similarity 68.9%; Pred. No. 2.8e-106;
Best Local Similarity 68.9%; Pred. No. 2.8e-106;
Matches 437; Conservative 25; Mismatches 58; Indels 114; Gaps 10;
Matches 437; Conservative 25; Mismatches 58; Indels 114; Gaps 10;
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                                                                                             ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                          EEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
                                           EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                             -- VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR
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PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                           PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP
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RESULT 20
AAE37574
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition preventing HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig; human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection; D2; alpha tailpiece; alphatp; fusion protein.
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DB; AAD29113.
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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08-AUG-1994
                                                             07-AUG-1992;
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                                        NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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WQQGNVFSCSVMHEALHNHYTQKSLSLSAGKPTHVNVSVVMAEVDGTC
                                                                                         ELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
                                                                                                                                                                                 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD
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AAR46679 standard; protein; 530 B

(revised) (first en entry)

CD4; gamma; heavy chain; chimeric; chimaeric; immunoconjugate; HIV; human immunodeficiency virus; radionuclide; toxin; therapy; treatment; imaging; detection; targetting; immunoglobulin; IgG.

92US-00927931 93WO-US007422 424. .530 /label= CF 205. .302 /label= CH1 Region. /label= CD4 Region. Location/Qualifiers /label= /label= Hinge Region . 423 CH3 Region CH2 Region

(PROG-) PROGENICS PHARM INC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image stage HIV infection.
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                                                                                                                                                                                                                                                                                                        ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                        EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAG---SGNL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                         DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                     EEQFNSTFRVVSVLTVVHQDWLNGKQYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                  -- VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                                                                                                                       PVWVLNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLALEAKTGKLHQEVNLVVMRATQL-QKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREK
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                                                                                                                                                                                                                                                                                                                                                                             -----SNTKVDKTVERKCCVECPPCPAPP-
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Pred. No. 9.8e-106;
8; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 255
                                         625
529
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ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL

120

ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLTIKNLKIEDSDTYICEVEDQKEEVQL

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                                                                                                                                  The invention relates to a CD4 (cluster of differentiation factor 4) polypeptide ligated at its C-terminus with a portion of an immunoglobulin (Ig) comprising a hinge region and a constant domain of a mammalian Ig heavy chain. The polypeptide comprises a tailpiece from the C-terminus of the heavy chain of an IgA or IgM antibody. Polypeptides of the invention are useful for preparing a composition for treating or preventing human immunodeficiency virus (HIV)-1 infection. The invention is useful in gene therapy and also in the preparation of vaccines. The present sequence is a fusion protein variant (G218P/L219V/220deLA/G321A) which comprises a human IgA alpha tailpiece (alphatp), a human IgG2 constant region comprising a hinge, a CH2 and CH3 region and a human CD4 DID2 domain. This variant protein is also referred to as mutant F
                                                                                                                                                                                                                                                                                                                                                New CD4 polypeptide ligated at its C-terminus with immunoglobulin, useful for preparing a composition preventing HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
Misc-difference 221
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-441545/41.
N-PSDB; ACC82877.
                                                                                                                                                                                                                                                                                                                      Example 11; Page 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; CD4; cluster of differentiation factor 4; immunoglobulin; Ig;
human immunodeficiency virus; gene therapy; vaccine; HIV-1 infection;
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                                                                     Similarity
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               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                        Conservative
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219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild type Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                  61.2%;
                                                                                                                                                                                                                                                                                                                     100pp; English.
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                                                  Score 2088; Ub .,
pred. No. 7.7e-105;
                                                     Pred. No. 7.70
3; Mismatches
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                       22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
                                                                                                                                                                                                                                                                                    AAB19510
                                                                             07-JUN-1995;
                                                                                              12-SEP-2000
                                                                                                               US6117656-A
                                                                                                                                                                   Key
                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                               CD4; IgM; human;
                                                                                                                                                                                                                                CD4-IgM
                                                                                                                                                                                                                                                  09-JAN-2001
                                                                                                                                                           Protein
       (GEHO)
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                                                                                                                                                                                                      diagnosis.
                                                                                                                                                                                                                                                                                      standard;
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                                                                                                                                                                                                                                                                                                                                                                                                    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                        LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPEL----LGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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       HOSPITAL
                                                                                                                                                                                                                                                  (first entry)
                       88US-00147351.

89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
                                                                              95US-00479353
                                                                                                                                         /note=
                                                                                                                                                                  Location/Qualifiers
                                                                                                                                 /note=
                                                                                                                                                                                                               CD4 Pmu;
                                                                                                                                                                                                                                                                                    protein; 481
       CORP
                                                                                                                                 "IgM heavy chain partial sequence"
                                                                                                                                                  "CD4 extracellular region"
                                                                                                                                                                                                               fusion
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                                                                                                                                                                                                               protein; immunoglobulin; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SADKTHTCPPCPAPPVAG
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                                                                                                                                                                                                                SIV;
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The present sequence is that of fusion protein CD4Pmu comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to the human IgM heavy chain. To obtain the fusion protein, DNA encoding CD4 was linked to IgM DNA at the Pst site upstream of the CH2 region (see AAA50663). Fusion protein CD4Pmu and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgM fusion proteins such as CD4Pmu provide complement-
                                          Sequence 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-586558/55
N-PSDB; AAA50662.
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                                                                                    mediated immunity
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Length
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                                                                                                                                                                                                QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
 EQYNSTYRVVSVLTV
                                                        VFLFPPKPKDTLMIS-RTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR----E
                                                                                     LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV-----
                                                                                                     LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLG--GPS
                                                                                                                                          LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                       LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                                                                                       TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                     TWTCTVLQNQKKVEFKLDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
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                               VSVFVP-
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                              -PRDGFFGNPRKSKLICQATGFSPR--QIQVSWLREGKQVGSGVTTDQVQAEAK
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Pred. No. 5.4e-104;
9; Mismatches 36;
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AAY59171 standard;

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                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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DB; AAZ48204.
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             LEAKTGKLHQEVNLVVMRATQLQKNLTCEVMGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
                                                                  QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                             TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELMW 240
                                                                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSJQFHWKNSNQIK
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                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 54-60;
                                                                                                                                                                                                                                                                                                                                   60.7%;
llarity 84.0%;
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Pred. No. 5.4e-104;
9; Mismatches 36;
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S 밁 Ś

13

| ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL

Similarity 83.8 L5; Conservative

18;

Indels

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  Query Match
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Matches 415
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                       This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a mino acids 1-174 or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gpl20. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Pmu which is constructed from CD4 linked
                                                                                                                Sequence 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion
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                                                                                                                                                                   IgM upstream
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89US-00299596.
92US-00896781.
93US-00057952.
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                         60.5%;
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                                                                                                                                                                protein CD4Pmu which of the CH2 region
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Score 2067; DB 3;
Pred. No. 1.1e-103;
8; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481
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                                                Length 481;
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RESULT 26
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The fusion protein genes of the invention pref. comprises cDNA which encode CD4 or a fragment which binds gp120 ligated to an plasmid which encodes an antibody in which the variable region gene has been deleted (see wo87-02671). The CD4 portion of the protein may comprise the complete CD4 sequence, the 370 AA extr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein;
diagnosis; CD4;
                                                                                                                                                                                                                                                           WPI; 1989-214472/30.
N-PSDB; AAN90359.
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03-AUG-1992
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                                                                                                                                              Example;
                                                                                                                                                                                      Immunoglobulin-CD4 fusion proteins - used infections or detecting HIV or SIV in samp
                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JAN-1989;
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m of the CH2
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                                                                                                                                         Table 4, Page 41-47; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                            HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     88US-00147351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89EP-00100913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin-like molecule; HIV; SIV;
gp120; binding fragment; glycoprotein; v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which encodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codes CD4 linked to human IgM (fusion protein CD4Pmu).
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n sample.
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variable
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       to an expression egion of the fusion A extracellular
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RESULT 27
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Best Local Similarity
Matches 415; Conserv
                                                                                                                                                                                                                                                                                                                                                       24-OCT-2003
25-MAR-2003
06-FEB-1993
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                                                                                                                                                                                                                                    homodimer; chimeric; :
                                                                                              Key
Domain
                                                                                                                                                                   Homo sapiens
Chimeric.
                                                Domain
                                                                                                                                                                                                                                                                                                        CD4-gamma2
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                                                                                                                                                                                                                                            increased
                                                                                                                                                                                                                                         soluble CD4; T
increased serum
                                                                                                                                                                                                                                                                                                           chimeric heavy chain homodimer.
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(revised)
(first en
Location/Qualifiers
1. .216
/label= CD4
217. .325
/label= CH2
326. .433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                       entry)
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                                                                                                                                                                                                                                         cell receptor; half life; HIV
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Pred. No. 1.4e-103;
9; Mismatches 37;
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                                                                                                                                                                                                                                            CD4 antigen;
infection; A:
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AIDS; ss.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a CD4-gamma2 chimeric heavy chain homodimer. It was produced by expression of the coding mutagenised cDNA (produced as described in AAQ28088) in Dhfr-CHO cells. The protein is efficiently assembled intracellularly and effectively secreted from mammalian cells pref. CHO, COS, or myeloma cells as a homodimer, enabling high recovery and purification from the medium of cells expressing it. It possesses increased serum half-life and has increased avidity for HIV of. heavy chain dimers. It can inhibit HIV infection of CD4+ cells and block the spread of HIV infection within a patient. Attachment to a detectable marker makes it useful in an assay for HIV or SIV infection, and it can also be linked to toxins, eg Diphtheria, Pseudomonas extoxin A (domains I or II) or the deglycosylated A-chain of ricin. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 432 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4-gamma-2 and CD4-IgG2 chimera(s) and expression vectors treatment, prevention and diagnosis of HIV infection.
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                                                                                                                                                                                                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW 240
                                                                                                                                                                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fig 3; 90pp; English
                   LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                         LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF 420
                                                                                                                                                      LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV 360
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                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAFERKCCV----
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Pred. No. 2.7e-103;
2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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        toxin or a gamma radiation-emitting radionuclide of low to moderate cytotoxicity. The resulting immunoconjugate comprising the toxin can be used to kill HIV infected cells and to treat HIV infected subjects to reduce the population of HIV infected cells. It can also be used to reduce the likelihood of infection. The immunoconjugate comprising the radionuclide can be used to image HIV infected tissue, to calculate the stage of HIV infection or the efficacy of an anti-HIV treatment using the imaging technique and for determining the prognosis of an HIV infected subject. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                     A CD4-gamma 2 chimeric heavy chain homodimer is linked to a non-
                                                                                                                                             Disclosure;
                                                                                                                                                                  Non-peptidyl toxin or radionuclide and CD4-gamma 2 or CD4-IgG2 immuno:conjugates - used to kill HIV-infected cells and to image HIV infection.
                                                                                                                                                                                                                                                       Allaway
                                                                                                                                                                                                                                                                                                       07-AUG-1992;
                                                                                                                                                                                                                                                                                                                               06-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD4; gamma;
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08-AUG-1994
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DB; AAQS7750.
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immunodeficiency virus; radionuclide;
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                                                                                                                                          Fig 3; 142pp; English.
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/label= Hinge Region
217. .325
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onuclide; toxin; therapy; treatme
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                                                                                                                  CD4-gamma 2 chimeric heavy chain homodimer; immunoconjugate; treatment; cytotoxic radionuclide; cell surface glycoprotein; prevent; infection; cellular immune response interaction mediator; HIV interaction; staging;
                                                                                                                                                                      Human CD4-gamma 2 chimeric heavy chain homodimer amino acid
 07-JUN-1995;
                         07-MAR-2000
                                                   US6034223-A.
                                                                           Homo sapiens
                                                                                                     prognosis; envelope glycoprotein burden;
                                                                                                                                                                                                19-JUN-2000
                                                                                                                                                                                                                                                    AAY85079
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                                                                                                                                                                                                                                                                                                                                                                                                                                       VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                   standard; protein;
                                                                                                                                                                                                                                                                                                                                            VFSCSVMHEALHNHYTQKSLSLSPG 625
                                                                                                                                                                                                                                                                                                                                                                    QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                                                                                                                                                                                                                                                                   VFSCSVMHEALHNHYTQKSLSLSPG 431
                                                                                                                                                                                                                                                                                                                                                                                                                           VVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
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 95US-00477460
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Pred. No. 2.7e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer CC immunoconjugate comprising a cytotoxic radionuclide and a heterotetramer CC of two heavy chains and two light chains. The cytotoxic radionuclide is CC linked to either the heavy chains or the light chains, or to all four CC chains, directly or through a bifunctional chelator. Both heavy chains CC linked to either the heavy chains or the light chains are chimeric CD4-kg-CC (ATCC 75193) and both light chains are chimeric CD4-kappa CC chains encoded by vector CD4-kLC-pRcCMV (ATCC 75193) and both light chains are chimeric CD4-kappa CC chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a non-cc chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a non-cc chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a non-cc chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a non-cc chains encoded by vector CD4-kLC-pRcCMV (ATCC 75194). CD4 is a non-cc complex 
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Best Local S
Matches 410
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06-AUG-1993;
03-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 58pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heterotetramer of CD4-immunoglobulin chimeras
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents the human CD4-gamma 2 chimeric heavy chain dimer amino acid sequence. The invention relates to an
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                                                                                                                                                                                                                           121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                            61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410;
                                                                                                                                                                                                                                                                                              61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                        PROGENICS PHARM INC
                                                                                                                                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                 QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFERKCCV--
                                                                                                                               TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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93WO-US007422.
95US-00379516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60.3%; Score 2059; DB 3; 65.6%; Pred. No. 2.7e-103; rative 12; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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301

LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV

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RESULT 30
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                                                                                                                                                                                                                                                                          subject, co
comprising
kappalight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1992;
06-AUG-1993;
03-FEB-1995;
07-JUN-1995;
                                      The present invention relates to an immunoconjugate, comprising a cytotoxic radionuclide linked, directly or via a bifunctional chelator, to a heterocetramer having two chimeric CD4-IgG2 heavy chains encoded by an expression vector CD4-IgG2NC-PRCCMV and two chimeric CD4-kappa light chains encoded by an expression vector CD4-kLC-pRcMV. The invention is useful for killing human immunodeficiency virus (HIV)-infected cells, for the treatment and prevention of infection with HIV
  Sequence
                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CD4-gamma2
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                                                                                                                                                                                                                                                                             Immunoconjugate for treating human immunodeficiency virus-infected subject, consists of cytotoxic radionuclide linked to heterotetramer comprising two chimeric CD4-IgG2 heavy chains and two chimeric CD4-kappalight chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PROG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [mmunoconjugate;
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93WO-US007422.
95US-00379516.
95US-00477460.
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Query Match

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Matches 410; Conserv
         08-FEB-1991;
10-FEB-1992;
08-DEC-1992;
                                                     07-JUN-1995;
                                                                           13-FEB-2001.
                                                                                               US6187748-B1
                                                                                                                     Homo
                                                                                                                                                      Human;
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                                                                                                                                          Human; Anti-HIV; CD4-IgG2 immunoglobulin gamma 2.
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         91US-00653684.
92WO-US001143.
92US-00960440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric heterotetramer to form a complex with the HIV (CD4 = cluster of differentiation 4; IgG2 = immunoglobulin gamma 2). CD4 is a cell surface glycoprotein that is expressed primarily on the surface of T cells. In man, CD4 is the target of interaction with HIV. The heterotetramer has two heavy and two light chains which are encoded by expression vectors CD4-IgG2HC-pRcCMV (V1) and CD4-kLC-pRcCMV (V2), respectively. The method is used to inhibit infection of a CD4+ cell by a HIV and to prevent CD4+ cells of a subject from becoming infected with HIV. The method is also useful for treating a subject having CD4+ cells infected with HIV. The present sequence is human fusion protein: CD4-gamma2 chimeric heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting human immunodeficiency virus (HIV) infection of a CD4+ cell, or treating a subject having CD4+ cells infected with HIV involves usin CD4-IgG2 chimeric heterotetramer to form a complex with the HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method for inhibiting infection of a CD4+ cell by HIV. The method comprises contacting the HIV with a CD4-IgG2
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                     QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGN
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                                                                                       VVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKN
                                                                                                                                                      LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432 AA;
QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRWQQGN
                                                                                                                                     LFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFR
                                                                                                                                                                                                                                     LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
                                                                                                                                                                                                                                                                                                                                                                         QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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Pred. No. 2.7e-103;
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RESULT 32
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10-FEB-1992;
08-DEC-1992;
                                                                   The invention describes a purified CD4-immunoglobulin (Ig)G2 chimeric heterotetramer (I) that neutralises human immunodeficiency virus-1 (HIV-1) having two heavy chains encoded by an expression vector designated CL-IgG2HC-pRcCMV, and two light chains encoded by expression vector designated CD4-kLC-pRcCMV. (I) and a composition (II) comprising (I) or (I) linked to a toxin, are useful for inhibiting HIV infection of a CD4 cell, and preventing a subject being infected with HIV by blocking the spread of HIV infection. This is the amino acid sequence of the CD4-gamma2 chimeric heavy chain of the CD4-IgG2 chimeric heterotetramer useful in inhibiting HIV infection
                                                                                                                                                                                                                                            Novel CD4-immunoglobulin G2 chimeric heterotetramer neutralizes human immunodeficiency virus-1 with two heavy and light chains encoded by expression vectors designated CD4-IgG2HC-pRcCMV and CD4-kLC-pRcCMV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD4;
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92US-00960440.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     = "Mature CD4-gamma2 chimeric chimeric heterotetramer"
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Score 2059; DB 6;
Pred. No. 2.7e-103;
2; Mismatches 9;
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RESULT 33
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion protein; human; CD4; IgM; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Mg.
  WPI; 2000-085792/07
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92US-00896781.
93US-00057952.
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                                                                                                SASAPTLF-----PLVSC
                                                LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHADPECPXPKPTPKAKLSTPSARTPG
                                                                   LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPV----PCPAPEPKSCDKTHT----CPE
                                                                                                                                                                                                                                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                       LLGGPSVFLFPPKPKDTLMISRTPEVTC
                                                                                                                                                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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Pred. No. 1.3e-102;
4; Mismatches 16;
433
                         440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of human immunodeficiency virus.
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RESULT 34
AAY59170
Homo
                                      HIV; extracellular; CD4; gp120; immunoglobulin; secreted protein; SIV infection; medicament.
                                                          CD4-Ig
                                                                        14-MAR-2000
                                                                                     AAY59170
                                                                                                   AAY59170 standard; protein;
                   sapiens
                                                           fusion
                                                          protein CD4Mmu
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Ig;

fusion

protein;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gpl20 when fused to an immunoglobulin (1g) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence which encodes the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gpl20 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the fusion protein cD4Mmu where the CD4 is linked to human IgG1 at the Mst2 site upstream of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful the treatment of HIV or simian immunodeficiency virus infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 474 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                              QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA 300
                                                                                                                                                                                                                                                                                                                                                                                                                   | ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                 LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
                                                                                                                                                                                               QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
                                                                                                                                                                                                                                                                                           TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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TCPPKPTPKAKLS-TPSARTPAPDLS 442
                             LFPPKPKDTLMISRTPEVTCVVVDVS 446
                                                             LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVHA---DPELPLTAHPKGQTLHSLSSD
                                                                                  LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSCDKTHTCPELLGGPSVF
                                                                                                                              LEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKPVWV
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                                                                                                                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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5; Mismatche
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2.8e-102;
nes 31;
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RESULT 35 AAR27278 ID AAR27

AAR27278

standard; protein; 532

180 120

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                                                                                                                                                                                                                                                                                                                               This sequence represents a fusion protein between the CD4 extracellular cd domain and the gamma protein membrane spanning domain and intracellular cd domain. The Fc-receptor-associated gamma chain is expressed in cell surface complexes with additional polypeptides, some of which mediate cligand recognition, and others which have undefined function. Gamma bears a homodimeric structure and overall organisation very similar to that of ceta (see also AAQ28704), and is a component of both the mast cell/basophil high affinity IgE receptor, Fc-epsilon-RI, which consists co fat least three distinct polypeptide chains and one of the low affinity creceptors for IgG, represented in mice by Fc-gamma-RII-alpha. In the production of the CD4 receptor chimera, the gamma cDNA was isolated from the HPB-ALL tumour cell line and from human natural killer cells. The gamma cDNA was joined to the extracellular domain by engineering a BamHI site naturally present a few residues upstream of the membrane spanning domain. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rusion protein; CD4; extracellular domain; zeta; eta; gamma; membrane spanning domain; intracellular domain; type I; integral membrane homodime; TCR; T cell antigen receptor; extracellular domain; mouse; human; receptor; chimera; HPB-ALL tumour cell line; natural killer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Therapeutic cells expressing chimeric receptors - or response to an infective agent, useful in treating Pneumocystis carinii infections etc.
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28-JUL-1995
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                                                                                                                                                                                                                                                                                                     Sequence 532
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                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                     ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                    Score 2036.5; DB 2
Pred. No. 5.5e-102;
1; Mismatches 3;
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g HIV-1, AIDS
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                                                                                                              Query Match
Best Local S
Matches 397
                                                                                                                                                                                        Fusion proteins comprising the extracellular domain of CD4 fused to T-cell receptor zeta, gamma or eta (AAR78676-78, respectively) were expressed in CV1 using a vaccine virus vector. These CD4:zeta, CD4:gamma and CD4:eta chimeric receptors mediated cytolysis of targets expressing
                                                                                                                                                                                                                                                                                                                                             Seed
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                                                                                                                                                           Sequence 532
                                                                                                                                                                                                                                                   Example
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N-PSDB; AAQ96124.
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02-AUG-1994;
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                                                                                                                                                                                                                                                                                    Target cytolysis of HIV-infected cells -
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                                                                              MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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94US-00284391.
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98.3%;
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AAT10801-T10803 represent membrane bound proteinaceous chimeric receptors of the invention. This sequence represents the CD4:eta chimera. The transmembrane region of the chimeric receptor acts to separate the intracellular and extracellular domains of the chimera, and contains a portion of the CD7 (see AAR89440), CD5 or CD34 transmembrane domains. Alternatively, the extracellular portion of the receptor can be separated from the intracellular domain by the hinge, CH2 and CH3 domains of human IgG1 (see AAR89441). The extracellular portion of the chimeric receptor contains a fragment of CD4 (amino acids 1-394 or 1-200 of the CD4 sequence, see AAR89450 and AAR89451) which specifically recognises and binds HIV-infected cells, but does not mediate HIV infection. The extracellular domain of the receptor is separated from the cell membrane by 48 or 72 angstroms, or by one or more proteinaceous alpha-helices. The cells expressing the receptor are preferably T cells, B cells, neutrophils, or dendritic cells. The therapeutic cells expressing the
                                                                                                                                                                                                                                                                                      Membrane-bound chimeric receptor comprising extracellular including CD4 fragment - cells expressing receptor can be treatment of HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                   Seed
                                                                                                                                                                                                                                                       Example 2; Page 80-81; 134pp; English
                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-129034/13.
N-PSDB; AAT10803.
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24-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9603883-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD7; transmembrane domain; chimeric receptor; CD5; CD34; CH2; CH3; IgG1; human; CD4; HIV; proteinaceous alpha-helix; T cell; B cell; neutrophil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dendritic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD4:eta fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banapour B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNPEAGMWQCLLSDSGQVLLESNIKVLPTWSTPVPCPAPEPKSC 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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95US-00394388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; mammal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
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RESULT 38
AAW83141
ID AAW83
XX AAW83
AC AAW83
AC Chime
CChime
XX Human
KW Human
KW CD4;
W CD4;
W CD584
XX O1-DE
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Best Local S
Matches 397
                                                                                                                                                                                      07-MAR-1991;
06-MAR-1992;
28-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; zeta; eta; gamma; membrane-bound chimeric receptor; infectumour; cancer cell; autoimmune-generated cell; T cell receptor; CD4; B cell receptor; Fc receptor; pathogen; bacterial; fungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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    Membrane-bound chimeric
                                                                                                                                                                                                                                                                       05-APR-1995;
                                                                                                                                                                                                                                                                                                                01-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         protozoan; viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric receptor containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW83141
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                                                                                                                                               (GEHO )
                                                                1999-044582/04
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397; Conserv
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                                            AAV70157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor are administered to a mammal to treat HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                    Kolanus W,
                                                                                                                                                 HOSPITAL
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92US-00847566.
94US-00203866.
                                                                                                                                                                                                                                                                       95US-00417495
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                                                                                                                                                 CORP
receptors - comprising extracellular portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human eta
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Pred. No. 5.5e-102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c receptor; infection;
T cell receptor; CD3;
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ARESULT 39
AAR27276
ID AAR27
XX AR27
AC AAR27
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DT 28-JU
XX CD4:2
XX CD4:2
XX Pusic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes DNA encoding a membrane-bound chimeric receptor comprising: (a) an extracellular portion that specifically recognises and binds a target cell or a target infective agent; and (b) an intracellular portion of a T-cell receptor CD3, zeta or eta polypeptide, a B-cell receptor polypeptide or an Fc receptor polypeptide. The present sequence represents a chimeric receptor containing the human eta polypeptide. Cells expressing chimeric receptors of the present invention can be administered to mammals in order to destroy pathogens (e.g. bacteria, fungi, protozoa or viruses, especially HIV), cancer cells
                Key
Protein
                                                                                           Pusion protein; CD4; extracellular domain; zeta; eta; gamm membrane spanning domain; intracellular domain; type I; integral membrane homodimer; TCR; T cell antigen receptor; extracellular domain; mouse; human; receptor; chimera; HPB-ALL tumour cell line; natural killer cell.
                                                                                                                                                                                                                           25-MAR-2003
28-JUL-1995
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                                                                                                                                                                                           CD4:zeta peptide chimeric protein
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                                                                                                                                                                                                                                                                                                         AAR27276 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which recognises and binds a target cell
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